

## Swope, Sheridan

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**From:** Page, Thurman  
**Sent:** Wednesday, March 30, 2005 6:35 PM  
**To:** Swope, Sheridan; STIC-Biotech/ChemLib  
**Cc:** Chan, Christina; Page, Thurman  
**Subject:** RE: 10/701,200

**Importance:** High

RUSH SEARCH APPROVED

Thurman K. Page  
SPE, Art Unit 1615  
Technology Center 1600  
571-272-0602

63-31-05

copy  
yes  
page

-----Original Message-----

**From:** Swope, Sheridan  
**Sent:** Wednesday, March 30, 2005 6:34 PM  
**To:** Page, Thurman  
**Cc:** Chan, Christina  
**Subject:** FW: 10/701,200

Ed. Hart

Chris didn't answer.

-----Original Message-----

**From:** Swope, Sheridan  
**Sent:** Wednesday, March 30, 2005 3:54 PM  
**To:** Chan, Christina  
**Subject:** 10/701,200

chris, may i have this rushed?

For 10/701,200, pls search and interference search:

SID 6 against the NT and AA data bases.

Thanks!

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E02B71 Remsen Bld (Office)  
E02C70 Remsen Bld (Mailbox)

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2005, 09:59:14 ; Search time 227 Seconds  
(without alignments)  
3150.013 Million cell updates/sec

Title: US-10-701-200-6

Sequence: 1 DVTWPHYHRLADIRFCMHWF.....FNSMLSEIGQPKGKGVESH 437

## Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-DB=Issued\_Patents\_NA -QPMT=fastap -SUFFIX=rnt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO\_MMAP -LARGEODERY\_NEG\_SCORES=0 -WAIT -DEPBLCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA:\*  
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3: /cgnt\_6/prodata/1/ina/6A.COMB.seq:\*  
4: /cgnt\_6/prodata/1/ina/6B.COMB.seq:\*  
5: /cgnt\_6/prodata/1/ina/PCUS.COMB.seq:\*  
6: /cgnt\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2284	100.0	1311	4	US-09-934-901-15
2	2284	100.0	1311	4	US-09-934-968-8
3	2284	100.0	1311	4	US-10-321-210-15
4	2284	100.0	1311	4	US-10-320-874-45
5	270	11.8	1778	1	US-08-416-870C-3
6	264.5	11.6	1624	1	US-08-416-870C-5
7	262	11.5	1978	1	US-08-416-870C-1
8	261	11.4	1038	4	US-09-902-540-8974
9	261	11.4	10391	4	US-09-902-540-858
10	260	11.4	1558	1	US-08-416-870C-9
11	246.5	10.8	2964	4	US-09-614-221A-404
12	239.5	10.5	6196	4	US-09-902-540-788

13	228	10.0	7972	4	US-08-956-171E-312	Sequence 312, App
14	228	10.0	7972	4	US-08-781-986A-312	Sequence 312, App
15	227	10.1	7972	4	US-09-489-039A-5087	Sequence 5087, App
16	226.5	9.9	1038	3	US-09-134-001C-937	Sequence 937, App
17	226.5	9.9	4244	4	US-09-710-279-4256	Sequence 4256, App
18	223	9.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
19	223	9.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
20	222.5	9.7	1008	4	US-09-583-110-2438	Sequence 2438, Ap
21	222.5	9.7	1006	4	US-09-502-540-7871	Sequence 7871, Ap
22	220	9.6	966	4	US-09-543-681A-4165	Sequence 4165, Ap
23	218.5	9.6	966	4	US-09-134-000C-1927	Sequence 1927, Ap
24	217.5	9.5	19446	3	US-08-961-527-51	Sequence 51, Appl
25	215.5	9.4	972	4	US-09-107-532A-2816	Sequence 2816, Ap
26	212.5	9.3	4605	3	US-09-221-0178-128	Sequence 128, App
27	211.5	9.3	2048	1	US-08-416-870C-7	Sequence 7, Appli
28	210.5	9.2	640681	4	US-09-790-988-1	Sequence 1, Appli
29	210	9.2	2510	4	US-09-949-016-3617	Sequence 3617, Ap
30	208.5	9.1	2880	4	US-09-614-221A-354	Sequence 354, App
31	206.5	9.0	3047	1	US-08-280-690-1	Sequence 1, Appli
32	204.5	9.0	2591	4	US-09-023-655-1414	Sequence 1414, Ap
33	204.5	9.0	2591	4	US-09-814-915A-102	Sequence 102, App
34	204.5	9.0	2591	4	US-09-949-016-380	Sequence 380, App
35	203.5	8.9	1274	4	US-09-887-054-1	Sequence 1, Appli
36	202.5	8.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
37	202.5	8.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
38	201.5	8.8	2909	4	US-09-949-016-5225	Sequence 5225, Ap
39	195	8.5	580073	4	US-08-545-528D-1	Sequence 1, Appli
40	182	8.0	924	4	US-09-710-279-2121	Sequence 2121, Ap
41	181	7.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
42	181	7.9	1230230	4	US-09-438-185A-1	Sequence 1, Appli
43	179	7.8	1230230	3	US-09-438-185A-1	Sequence 105, App
44	176.5	7.7	2255	3	US-08-714-918-105	Sequence 105, App
45	176.5	7.7	2255	3	US-09-265-315-105	Sequence 105, App

## ALIGNMENTS

## RESULT 1

US-09-934-901-15  
; Sequence 15, Application US/09934901  
; Patent No. 6553533  
; GENERAL INFORMATION:  
; APPLICANT: Kofifas, Matheos  
; APPLICANT: Odum, J. Martin  
; APPLICANT: NO. 6555353ton, Kelley C.  
; APPLICANT: Ye, Rick  
; TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN  
; FILE REFERENCE: CL1619 US NA  
; CURRENT APPLICATION NUMBER: US/09/934, 901  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/229, 906  
; PRIOR FILING DATE: September 1, 2000  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 15  
; LENGTH: 1311  
; TYPE: DNA  
; ORGANISM: METHYLOMONAS SP.  
US-09-934-901-15

## Alignment Scores:

Pred. No.:	7.48e-264	Length:	1311
Score:	2284.00	Matches:	437
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-701-200-6 (1-437) x US-09-934-901-15 (1-1311)

Oy	1	AspValValThrTrpProtyrHisLeuThrAlaAspIleArgGlycysHisTrpPhe	20
Db	1	GAGTGTGTCACATGGCCCTTACCTTAACGGCTGATATTCGATTGTCATTGTTT	60

QY 21 LeuAsnPheAsnPhetYrThrLeuMetAsnLysProLysLysValAlaIleLeuThrAla 40  
 Db 61 CTAACTTTAACTTCAACGCTCATGACAAACCTAAAGTTTCAATCTACGACAGCA 120  
 QY 41 G1YGI1LeuAlaProCysLeuAsnSerAlaIleG1SerLeuIleGluArgYrThrGlu 60  
 Db 121 GCGCGCTGGCGCTTGTGTAATTCGCGAATCGGTAAGTTTGAATCCAACTTATACGAA 180  
 QY 61 IleAspProSerIleGluIleIleCysYrYrArgG1YGI1YrLysG1YLeuLeuLeuG1Y 80  
 Db 181 ATCGATCTCTAGCATAGAAATCAATTTGCTATCGCGCGGTTATTAAGGCGCTGTGGG 240  
 QY 81 AspSerTyrProValThrAlaGluValArgLysLysAlaG1YValLeuGlnArgPheG1Y 100  
 Db 241 GATTCTTATCCAGTAACGGCCGAAGCGCTTAAGAAAGCGGCGTTCGCAACCTTTTGGC 300  
 QY 101 G1YSerValIleG1YAsnSerArgValIleLeuThrAsnValIleAspCysValIleYrArg 120  
 Db 301 GGTTCGTGATCGGCAACGCCGCTCAATTAATGACCAATTCGCAAGCTGCGTAAGCG 360  
 QY 121 G1YLeuValIleG1YGI1YGI1YLeuAspProGlnLysValAlaIleAspGlnLeuValIleYrAsp 140  
 Db 361 GGTTCGTGATAAGGGTGAAGATCCGCAAAAGTGGCGCTGATCAATGGTTAAGAT 420  
 QY 141 G1YValAspIleLeuHisThrIleG1YGI1YAspAspThrAsnThrAlaAlaIleAspLeu 160  
 Db 421 GGTCGTGATATTCGACACCATCGCGCGGATGATACCAATCGCGACGCGGATTTG 480  
 QY 161 AlaAlaPheLeuAlaArgAsnAsnYrG1YLeuThrValIleG1YLeuProLysThrVal 180  
 Db 481 GCAGCATCTTCGGCCAGAAATTAATTCGAGCTACCGCTCATTTGTTTAAACCGTC 540  
 QY 181 AspAsnAspValPheProIleLysGlnSerLeuG1YAlaIleThrAlaAlaGlnGlnG1Y 200  
 Db 541 GATTAAGCATATTTCCGATCAAGCATATCTAGTGGCTTGGATCGCGCGGCAAGGC 600  
 QY 201 AlaArgTyrPheMetAsnValIleAlaGluAsnAsnAlaAsnProArgMetLeuIleVal 220  
 Db 601 GCGCGTTATTTCAAGAACGTGGTGGCGGAAACAAACCCCAACGCGCATGCTGATGTA 660  
 QY 221 HisGluValMetCysArgAsnG1YrLysLeuThrAlaAlaThrAlaGlnGlnG1YrArg 240  
 Db 661 CAGGAAGTATGGGCGGTAATCTGCGCTGCTACCGCTGCAACCGGCGGGAATTCGG 720  
 QY 241 LysLeuLeuAspArgIleGluThrLeuProGlnLeuG1YLeuThrArgIleGlnSerTyrGln 260  
 Db 721 AATTATCTGACCGTGGCGGATGGTGGCGGAATGGGTTGATCGTGAATCTTATGA 780  
 QY 261 ValHisAlaValPheValProGlnMetAlaIleAspLeuGlnAlaGluValLysArgLeu 280  
 Db 781 GTCCAGCGGCTATTCGTTCCGGAATGGCGATGACCTGGAAACCGCAAGCCGCTG 840  
 QY 281 ArgGluValMetAspLysValAspCysValAsnIlePheValSerGlnGluAlaGluVal 300  
 Db 841 CGGGAAGTATGGACAAAGTCATGCGTCAACATCTTCGTTCCAAAGGTGCGGCGTC 900  
 QY 301 GluAlaIleValAlaGlnMetGlnAlaLysG1YGI1YGI1YValProArgAspAlaPheG1Y 320  
 Db 901 GAAGCTATGCTCGCGGAATGCAAGCGCAAGGCGCAAGAGTGGCGCGCATGCTTCGG 960  
 QY 321 HisIleLysLeuAspAlaValAsnProG1YrLysThrPheG1YGI1YGI1YLeuIleAlaGlnMet 340  
 Db 961 CATATCAATCGATGGGTCACACCTCGTAAATGTTGCGGAGCAATTCGCGCAGATG 1020  
 QY 341 IleG1YAlaGluLysThrLeuValGlnLysSerG1YrLysPheAlaArgAlaSerAlaSer 360  
 Db 1021 ATAGGCGCGGAAACCTCTGTGACAAATCGGGAATCTTCGCGGTCTTGTGCTTC 1080  
 QY 361 AsnValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPhe 380  
 Db 1081 AACGTTGACACATGCTTGTGATCAATCTGCGCGCATCTTGGCGGTGCAAGTGGCGCTTC 1140

QY 381 ArgArgGlnSerG1YValIleG1YHisAspGluAspAsnG1YAsnValLeuArgAlaIle 400  
 Db 1141 CCCCCGAGTCTGGGTGATCGGTACAGCAAGACAAACGCGAAGCTGTGGCGGATC 1200  
 QY 401 GluPheProArgIleLysG1YGI1YLysProPheAsnIleAspThrAspTrpPheAsnSer 420  
 Db 1201 GAGTTTCCGCGCATAGGCGCGCAACCGTTCAATATGACACCGACTGTTCAATAC 1260  
 QY 421 MetLeuSerGlnIleG1YGI1YGI1YLeuProLysG1YGI1YLysValGluValSerHis 437  
 Db 1261 ATGTTGAGCAATCGGCGCACGCTAAAGCGGTTAAAGTCGAAGTACGCCAC 1311  
 RESULT 2  
 US-09-934-868-5  
 ; Sequence 5, Application US/09934868  
 ; Patent No. 6689601  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kofas, Matheos  
 ; APPLICANT: Odem, James M  
 ; APPLICANT: Schenzle, Andreas J  
 ; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
 ; FILE REFERENCE: CL1596 US NA  
 ; CURRENT APPLICATION NUMBER: US/09/934,868  
 ; PRIORITY FILING DATE: 2001-08-22  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 5  
 ; LENGTH: 1311  
 ; TYPE: DNA  
 ; ORGANISM: METHYLOMONAS SP.  
 US-09-934-868-5  
 Alignment Scores:  
 Pred. No.: 7,486-264 Length: 1311  
 Score: 2284.00 Matches: 437  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0  
 US-10-701-200-6 (1-437) x US-09-934-868-5 (1-1311)  
 QY 1 AspValValThrTrpProTyrHisLeuThrAlaAspIleArgPheCysHisTrpPhePhe 20  
 Db 1 GATGGTGCATATGGCCCTATCATCTTAACGGCTGATTCGATTTGTGATGTTT 60  
 QY 21 LeuAsnPheAsnPhetYrThrLeuMetAsnLysProLysLysValAlaIleLeuThrAla 40  
 Db 61 CTAACTTTAACTTCAACGCTCATGACAAACCTAAAGTTTCAATCTACGACAGCA 120  
 QY 41 G1YGI1LeuAlaProCysLeuAsnSerAlaIleG1SerLeuIleGluArgYrThrGlu 60  
 Db 121 GCGCGCTGGCGCTTGTGTAATTCGCGAATCGGTAAGTTTGAATCCAACTTATACGAA 180  
 QY 61 IleAspProSerIleGluIleIleCysYrYrArgG1YGI1YrLysG1YLeuLeuLeuG1Y 80  
 Db 181 ATCGATCTCTAGCATAGAAATCAATTTGCTATCGCGCGGTTATTAAGGCGCTGTGGG 240  
 QY 81 AspSerTyrProValThrAlaGluValArgLysLysAlaG1YValLeuGlnArgPheG1Y 100  
 Db 241 GATTCTTATCCAGTAACGGCCGAAGCGCTTAAGAAAGCGGCGTTCGCAACCTTTTGGC 300  
 QY 101 G1YSerValIleG1YAsnSerArgValIleLeuThrAsnValIleAspCysValIleYrArg 120  
 Db 301 GGTTCGTGATCGGCAACGCCGCTCAATTAATGACCAATTCGCAAGCTGCGTAAGCG 360  
 QY 121 G1YLeuValIleG1YGI1YGI1YLeuAspProGlnLysValAlaIleAspGlnLeuValIleYrAsp 140  
 Db 361 GGTTCGTGATAAGGGTGAAGATCCGCAAAAGTGGCGCTGATCAATGGTTAAGAT 420  
 QY 141 G1YValAspIleLeuHisThrIleG1YGI1YAspAspThrAsnThrAlaAlaIleAspLeu 160

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Db      421 GGGTGGATTTCTGCACACATCGCGGAGATACCAATCGCGACGAGGATTTG 480
Qy      161 ALaAlaPheLeuAlaArgAenAntYrGlyLeuThrValIleGlyLeuProlySerThrVal 180
Db      481 GCAGCATTCCTGGCCGAAATTAATTAACGACTAACCGCTCATTTGTTTAAACCGTTC 540
Qy      181 AspAenAspValPheProIlelysgInserLeuGlyValaIleThrAlaIleagIngly 200
Db      541 GATPACGAGTATTTCCGATCAAGCAATCATAGTCTTGGATCGCCGCGAGCAAGGC 600
Qy      201 AlaArgTyPheMetAenValValaIleGluAenAsnAlaAsnProArgMetLeuIleVal 220
Db      601 GCCCGTTATTTCTGAAACGTGGCGGCAAAACACCCCAACCGCATGCTGATCGTA 660
Qy      221 HsGluValMetGlyYrGAsnCyGlyTrpLeuThrAlaIleThrAlaIleagInglyYrArg 240
Db      661 CACGAAGTATGGGCGGTAACTCGGCTGGCTGACCGCTGCAACCGCGAGGAATATCGC 720
Qy      241 LylLeuLeuAspArgAlaGluTrpLeuProGluLeuGlyLeuThrArgInserTyrglu 260
Db      721 AATTTACTGACCGTGGCGAGTGGTGGCGAATGGGTTTGACTGTGAATCTTATGAA 780
Qy      261 ValHsAlaValaPheValProGluMetAlaIleAspLeuGluAlaGluAlaIlySerGly 280
Db      781 GTGCACGCGGTATTCGTTCCGAAATGGCGATCGACCTGGAAACCGCAAGCCGCTG 840
Qy      281 ArgGluValMetAspValAspValaAsnIlePheValSerGluGlyValaIleVal 300
Db      841 CGCGAAGTATGGACAAAGTCATGCGTCAACATCTTCGTTCCGAAGGTGGCGGCTC 900
Qy      301 GluAlaIleValaIleGluMetGlnAlaIlyGlyGluValaProArgAspAlaPheGly 320
Db      901 GAAAGTATCTCCCGGAAATGCAAGCCCAAGGCAAGGATGCCCGCATGCTTCGCGC 960
Qy      321 HsIlelyLeuAspAlaValaAsnProGlyYrTrpPheGlyGluGlnPheAlaGlnMet 340
Db      961 CACATCAAACTGGATCGGTCGATCAACCTCGTAAATGTTCCGCGAGCAATTCGCGCAGATG 1020
Qy      341 IleGlyAlaGlyYrThrLeuValGlnIlySerGlyTyTrpPheAlaArgAlaSerAlaSer 360
Db      1021 ATAGGCGGGAATAAACCTCGTGAATAAAATCGGAAATCTTCGCGTCTTGTGCTCC 1080
Qy      361 AsnValaAspAspMetArgLeuIlelySerCysAlaAspLeuAlaValaGluCysAlaPhe 380
Db      1081 AACGTTGACGACATGCTTGGATCAATCTGCGCCGACCTTGGCGGTGCGATCGCGCTTC 1140
Qy      381 ArgArgGluSerGlyValIleGlyYrHsAspGluAspAsnGlyAsnValaLeuArgAlaIle 400
Db      1141 CGCGCGAGTCTGGCGTATCGGTCACGACGAAGACAAACGCGCAACGTGTTGCGCGATC 1200
Qy      401 GluPheProArgIlelysgIlyYrPhePheAsnIleAspThrAspTrpPheAsnSer 420
Db      1201 GAATTTCCGGGCAATCAAGGCGGCAACCGTTCAATATCAACACGATCGGTTCAATAGC 1260
Qy      421 MetLeuSerGluIleGlyGlnProlyGlyGlyYrValaGluValaSerHis 437
Db      1261 ATGTTAGCAAAATCGCCACGCTTAAGCGGTAAAGTCAAGTCAAGCCAC 1311

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; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,906
; PRIOR FILING DATE: September 1, 2000
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: METHYLOMONAS SP.
US-10-321-210-15

Alignment Scores:
Pred. No.: 7,48e-264 Length: 1311
Score: 2284.00 Matches: 437
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
DB: 4

US-10-701-200-6 (1-437) x US-10-321-210-15 (1-1311)

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Qy      21 LeuAsnPheAsnPhetyrThrLeuMetAenIysProlyValaValaIleLeuThrAla 40
Db      61 CTTAACTTTAACTTCTACACGCTCAAGAACAAACCTAAABAAAGTTCCATATCGACAGCA 120
Qy      41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGluArgTyrglu 60
Db      121 GCGGCGCTTGCGCTTGTGAATTCGCAATCGGATGTTATCGAACGTTATACGAA 180
Qy      61 IleAspProSerIleGluIleIleCysTyrgArgGlyTyTrpIlyGlyLeuLeuGly 80
Db      181 ATGATCTTACGATCAATAAAATCTTGTCTATCGCGGCTTATTAAGCCCTGTGCTGCGC 240
Qy      81 AspSerTyProValThrAlaGluValaArgIlyValaIleGluGlnArgPheGly 100
Db      241 GATTTCTTACCAATACGCGCCGAAGCGCTTAABAAAGCGGCTTCTGCACTTTGGC 300
Qy      101 GlySerValIleGlyAsnSerArgValIlyLeuThrAsnValIlyAspCysValIlyArg 120
Db      301 GGTTCGTGATCGGCAACGCGCGTCAATGACCAATGTCAAAGATCGCGTGAACCGC 360
Qy      121 GlyLeuValIlyGlyGluIlyGluAspProGluIlyValaAlaAlaAspGluIlyAsp 140
Db      361 GGTTCGTCAAGAGGATGAAGATCGCAAAAGTCCGCGTGAATCTTGTGAAGAT 420
Qy      141 GlyValaAspIleLeuHsIleThrIleGlyYrAspAspThrAsnThrAlaAlaAspLeu 160
Db      421 GGTTGCAATTTCTGCACACCATCGCGCGATGATACCAATACGCGACGACGAGTTTG 480
Qy      481 AlaAlaPheLeuAlaArgAenAntYrGlyLeuThrValIleGlyLeuProlySerThrVal 180
Db      181 GCAGCATTCCTGGCCGAAATTAATTAACGACTAACCGCTCATTTGTTTAAACCGTTC 540
Qy      181 AspAenAspValPheProIlelysgInserLeuGlyValaIleThrAlaIleagIngly 200
Db      541 GATPACGAGTATTTCCGATCAAGCAATCATAGTCTTGGATCGCCGCGAGCAAGGC 600
Qy      201 AlaArgTyPheMetAenValValaIleGluAenAsnAlaAsnProArgMetLeuIleVal 220
Db      601 GCCCGTTATTTCTGAAACGTGGCGGCAAAACACCCCAACCGCATGCTGATCGTA 660
Qy      221 HsGluValMetGlyYrGAsnCyGlyTrpLeuThrAlaIleThrAlaIleagInglyYrArg 240
Db      661 CACGAAGTATGGGCGGTAACTCGGCTGGCTGACCGCTGCAACCGCGAGGAATATCGC 720
Qy      241 LylLeuLeuAspArgAlaGluTrpLeuProGluLeuGlyLeuThrArgInserTyrglu 260
Db      721 AATTTACTGACCGTGGCGAGTGGTGGCGAATGGGTTTGACTGTGAATCTTATGAA 780

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QY 261 VAHIAIAVAIAPHEVAIProglumecAIAIleaspleuGluAgluaIalyaIgleu 280  
DB 781 GTGACGCGGTATTCCTTCGGAATGGCGATGACCTGGAAAGCCAAAGCCGCTG 840  
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DB 841 CCGGAAGTATGACAAAGTCGATTCGCTCAACATCTTCCTCCAGAGTCCGCGCTC 900  
QY 301 GluAlaIleValAlaGluMetGlnAlaIySerGluGluValProArgAspAlaPheGly 320  
DB 901 GAAGCTATCGTCGCGGAATGCAAGCCAAAGCCAGAAAGTCCGCGCATGCTTCGCG 960  
QY 321 HisIleIyLeuAspAlaValAsnProGluIySerPheGluGluGlnPheAlaGlnMet 340  
DB 961 CACATCAAACTGATCGGTCAACCTGTGTAATGTTGCGCAGCAAAATTCGCGCAGAG 1020  
QY 341 IlegIyAlaGluIySerThrLeuValGlnIySerGluIyPheAlaArgAlaSerAlaSer 360  
DB 1021 ATAGGCGCGGAATAAAACCTGGTACAAATTCGGGATACCTTCGCGCTTCCTTC 1080  
QY 361 AsnValAspAspMetArgLeuIleIySerCysAlaAspLeuAlaValGluCysAlaPhe 380  
DB 1081 AACGTGACGACATGCGTTGATCAATCGTCGCCGACTTGGCGGTGCGAGTCCGCTTC 1140  
QY 381 ArgArgGluSerGluValIlegIyHisAspGluAspAsnGluValLeuArgAlaIle 400  
DB 1141 CCGCGGAGTCTGCGCTGATCGGTCAAGCAGAAACAACCGCAACGTGTTCGCTGCATC 1200  
QY 401 GluPheProArgIleIySerGluIyLysProPheAsnIleAspThrAspTrpPheAsnSer 420  
DB 1201 GAGTTCCGCGCATCAAGGCGGCAACCTTCATATTCACACCGACTGTTCAATAGC 1260  
QY 421 MetLeuSerGluIleGluIyGlnProIyGluIyLysValGluValSerHis 437  
DB 1261 ATGTGAGCGCAATCGGCCAGCCTAAAGCGGTAAAGTGAAGTCAAGCCAC 1311

RESULT 4  
US-10-320-874-15  
Sequence 15, Application US/10320874  
Patent No. 6773905  
GENERAL INFORMATION:  
APPLICANT: Koffae, Matheos  
APPLICANT: Odom, J. Martin  
APPLICANT: No. 6773905ton, Kelley C.  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/10/320, 874  
CURRENT FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US/09/934,901  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,906  
PRIOR FILING DATE: September 1, 2000  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 15  
LENGTH: 1311  
TYPE: DNA  
ORGANISM: METHYLOMONAS SP.  
US-10-320-874-15

Alignment Scores:  
Pred. No.: 7,48e-264 Length: 1311  
Score: 2284.00 Matches: 437  
Percent Similarity: 100.00% Conservative: 0  
Beet Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-701-200-6 (1-437) x US-10-320-874-15 (1-1311)

QY 1 AsnValValThrTrpProIyThrIleuThrAlaAspIleArgPheCysHisIleTrpPhePhe 20  
|||||

DB 1 GATGTCGACATGGCCCTCATCTTAACGGCTGATTCATTCGATTTTCATTGCTTTT 60  
QY 21 LeuAsnPheAsnPheIyThrLeuMetAsnIySProIyLysValAlaIleuThrAla 40  
DB 61 CTTAATCTTAATCTTCTACACGCTCATGAACAAACCTAAABAAAGTTGCATATCTGACAGA 120  
QY 41 GlyIyLeuAlaProCysLeuAsnSerAlaIlegIySerLeuIlegIuArgIyThrGlu 60  
DB 121 GCGGCTTGGCCCTTGTGTGAATTCGCCAAATCGGTATGATGAAAGTTATACCGAA 180  
QY 61 ILeaPProSerIleGluIleIleCysIyTrArgIyGluIyLysGluIyLeuLeuGluIy 80  
DB 181 ATCGATCTCGATATGAATCAATCTTGTCTATCCGCGGCTTAATAAGCCTTGTCTGGGC 240  
QY 81 AspSerIyProValThrAlaGluValArgIyLysAlaGluValLeuGlnArgPheGly 100  
DB 241 GATTCCTTAATCCAGTAAAGCCGCAAGTGGGTAAAGGCGGCTTCGCAACGTTTGGC 300  
QY 101 GIservAlIlegIyAsnSerArgValIyLeuThrAsnValIyAspCysValIyArg 120  
DB 301 GGTTCGTGATCGGCAACGCGCGCTCAATGACCAATGTCAAAAGACTGCGTGAACCC 360  
QY 121 GIservValIlegIyLysGluIyLysAspProGluIyValAlaAspGlnIyValIyAsp 140  
DB 361 GGTTCGTCAAGAGGCTGAAGATCCGCAAAAGTCCGCGCTCATCAATGGTTAAGAT 420  
QY 141 GIservAlIlegIyAsnSerArgValIyLeuThrAsnValIyAspCysValIyArg 160  
DB 421 GGTTCGTCAATCTGACACCATCGCGCGCATGTATCAATATACGACACAGCGATTTG 480  
QY 161 AlaIlePheLeuAlaArgAsnArgIyGluIyLeuThrValIlegIyLeuProIySerThrVal 180  
DB 481 GCAGCATTCCTCGCCAGAAATTAATACGACACTGACCGCTATGTTTACCTAAACCCGTC 540  
QY 181 AspAsnAspValPheProIleIySerGlnSerLeuGluValATrPheAlaIleGluGlnIy 200  
DB 541 GATTAACGACGTATTCCTCGATCAAGCAATCACTAGTCTTGAACCTGCCGCGACAGGCG 600  
QY 201 AlaArgIyPheMetAsnValValAlaGluAsnAsnAlaAsnProArgMetLeuIleVal 220  
DB 601 GCGCGTTATTTATGATAAGCGTGTGCGCAAAACAACGCAACCATGCTGATCGTA 660  
QY 221 HisGluValMetGluArgAsnCysGluIyTrpLeuThrAlaIleThrAlaGlnIyTrArg 240  
DB 661 CACGAAGTATGCGCGCTGAATCTGCGCTGCGACCGCTGCACACCGCGCAGAAATTCGCC 720  
QY 241 LysLeuLeuAspArgAlaGluIyTrpLeuProGluLeuGluIyLeuThrArgGluSerIyGlu 260  
DB 721 AATTTACTGGACCGTGGCGAGTGTGGCGGAAATGGTTTACTGCTGTAATCTTATGAA 780  
QY 261 ValHisAlaValAPHEVAIProglumecAIAIleaspleuGluAgluaIalyaIgleu 280  
DB 781 GTGACGCGGTATTCCTTCGGAATGGCGATGACCTGGAAAGCCAAAGCCGCTG 840  
QY 281 ArgGluValMetAspIysValAspCysValAsnIIPheValSerGluGluVal 300  
DB 841 CCGGAAGTATGACAAAGTCGATTCGCTCAACATCTTCCTCCAGAGTCCGCGCTC 900  
QY 301 GluAlaIleValAlaGluMetGlnAlaIySerGluGluValProArgAspAlaPheGly 320  
DB 901 GAAGCTATCGTCGCGGAATGCAAGCCAAAGCCAGAAAGTCCGCGCATGCTTCGCG 960  
QY 321 HisIleIyLeuAspAlaValAsnProGluIySerPheGluGluGlnPheAlaGlnMet 340  
DB 961 CACATCAAACTGATCGGTCAACCTGTGTAATGTTTGGGAGCAAAATTCGCGCAGAG 1020  
QY 341 IlegIyAlaGluIySerThrLeuValGlnIySerGluIyPheAlaArgAlaSerAlaSer 360  
DB 1021 ATAGGCGCGGAATAAAACCTGGTACAAATTCGGGATACCTTCGCGCTTCCTTC 1080  
QY 361 AsnValAspAspMetArgLeuIleIySerCysAlaAspLeuAlaValGluCysAlaPhe 380  
DB 1081 AACGTGACGACATGCGTTGATCAATCGTCGCCGACTTGGCGGTGCGAGTCCGCTTC 1140

Qy 381 ArgArgGluSerGlyValIleGlyHisAspGluAspAsnGlyValAsnValIleuArgAlaIle 400  
Db 1141 CGCGCGAGCTGGCGGATCGGTCAGCAGCAGAACAGCAGTTCGGCGGATC 1200  
Qy 401 GluPheProArgIleLeuGlyGlyValProPheAsnIleAspThrAspTrpPheAsnSer 420  
Db 1201 GAGTTTCGGCGATCAAGGGCGGCAACCGTTCATATGACACCGACTGTTCAATAGC 1260  
Qy 421 MetLeuSerGluIleGlyGlnProLeuGlyGlyValGluValSerHis 437  
Db 1261 ATGTGAGCAAAATCGGCGACCTTAAGGCGGTAAAGTCAAGTCAGCCAC 1311  
RESULT 5  
US-08-416-870C-3  
Sequence 3. Application US/08416870C  
Patent No. 5824862  
GENERAL INFORMATION:  
APPLICANT: HIYOSHI, TORU  
APPLICANT: MINE, TOSHIKI  
APPLICANT: KASAKA, KEISUKE  
APPLICANT: TYSON, ROBERT HUI  
APPLICANT: PAGE, ANTHONY MILES JOHN  
TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE  
TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO  
TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
STREET: PO BOX 747  
CITY: FALL CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/416,870C  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 760-195P (PCT)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8000  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1778 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 19..1467  
US-08-416-870C-3  
Alignment Scores:  
Pred. No.: 5,29e-22 Length: 1778  
Score: 270.00 Matches: 113  
Percent Similarity: 40.59% Conservative: 53  
Best Local Similarity: 27.63% Mismatches: 175  
Query Match: 11.82% Indels: 68  
DB: 1 Gaps: 15  
US-10-701-200-6 (1-437) x US-08-416-870C-3 (1-1778)  
Qy 36 AlaIleuThrAlaGlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIle 55

Db 301 GCTATGATGAACATGCTGGTGTATATGCTGGGCTAAACACATGTATCAGGGAATATGTT 360  
Qy 56 GluArgTrpThrIuIleAspProSerIleGluIleCysTrpArgGlyTrpLeu 75  
Db 361 TGGCAGCTTATGATACATGATGCTGATCACCAGGTTCTGGGATGATGAGGGGTACAG 420  
Qy 76 GlyLeuLeuLeuGlyAspSerTrpProValThrAlaGluValArgHisLysAlaGlyVal 95  
Db 421 GGTTTTATGCAAAAACACCATCCTTGATGCTCCAAAGTT-----GTGAATGAC 471  
Qy 96 LeuGluArgPheGlyGlySerValIleGlyAsnSerArgValLysLeuThrAsnValLys 115  
Db 472 ATCATTAACGCTGGTGTACATTAATTTGGCACCCTCTCGT----- 510  
Qy 116 AspCysValLysArgGlyLeuValLysGluGlyAspProGlnLysValAlaAlaAsp 135  
Db 511 -----GGGGGCGATGATTAACCAAGATA--GTTGAC 540  
Qy 136 GluLeuValLysAspGlyValAspIleLeuHisThrIleGlyGlyAspAspThrAsnThr 155  
Db 541 AGTATTCAGATGCTGTATCATCATCAGCTTATATATATGAGAGACGCTACTCAAAAG 600  
Qy 156 AlaAlaAlaAspLeuAlaAlaPheLeuAlaArgAsnAsnTrpGlyLeuThrValIleGly 175  
Db 601 GAGCAGAGCTGTATTATACAGAAAGAGAGCGCTGCTTAAAGCTGTAGTGGCTGGG 660  
Qy 176 LeuProLysThrValAspAsnAspValPheProIleLysGlnSerLeuGlyAlaTrpThr 195  
Db 661 ATTCCTTAAGCAATTAATATATGACATTCGGCTATGATTAAGTCTTTGTTTGACACG 720  
Qy 196 AlaAlaGluGlnGlyAlaArgTrpPheMetAsnValAlaGluLysAsnAlaAsnPro 215  
Db 721 GCTGTGGAAGAGGCTCAAGCTGCCATTAAATGCTGCACATGTGAGGCTGAAGTCTGAG 780  
Qy 216 ArgMetLeuIleValHisGluValMetGlyArgAsnCysGlyTrpLeuThrAlaAlaThr 235  
Db 781 AATGGCATAGGGGTGTCNAACCTTATGGAGCGCTATATAGTATTCATTCGCA----- 831  
Qy 236 AlaGlnGluTrpArgLysLeuLeuAspArgAlaGluTrpLeuProGluLeuGlyLeuThr 255  
Db 832 -----ATGATGCAACT 843  
Qy 256 ArgGluSerTrpGluValHisAlaValPheValProGluMetAlaIleAspLeuGluAla 275  
Db 844 TTGGCTAGTGAAGATGTTATATGTTATCTTAAATCTCGAATCACCCTTTTATCTTGAGCA 903  
Qy 276 GluAla-----LysArgLeuArgGluValMetAspLysValAsp 288  
Db 904 GAAAGTGAGACTTTTGAATATGTAGAAAACGCTCAAGGACGATGACATGTC--- 960  
Qy 289 CysValAsnIlePheValSerGluGlyAlaGlyValAlaIleValAlaGluMetGln 308  
Db 961 -----ATCGTTGAGCAGAAAGGTGCTGTCAGAGCTGCTTCACGACGAAAACCTTG 1011  
Qy 309 AlaLysGlyGlnGluValProArgAspAlaPheGlyHisIleLysLeuAspAlaValAsn 328  
Db 1012 AAA-----ACTTCAAACCGCAAAAGATGCTTCGAAATAACTACTTACGAGTGC--- 1062  
Qy 329 ProGlyLysTrpPheGlyGluGln-----PheAlaGlnMetIleGlyAlaGlu 344  
Db 1063 ---GATGTGCGATTTCTGTATGATTAAGGCTCACCTTGCTTAATAATCTCCATGCGCT 1119  
Qy 345 LysThrLeuValGln---LysSerGlyTrpPheAlaArgAlaSerAlaSerAsnValAsp 363  
Db 1120 ATTACTCTCAATATACATAGATCCAACTTACATGATCCGTGCTCCAAATATGATCTT 1179  
Qy 364 AspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPheArgArgGlu 383  
Db 1180 GATTAAT-----GTATCTGCACTCTCTGCTCAAGTTGTCTTCAAGAGTGATG 1230  
Qy 384 SerGlyValIleGlyHisAspGluAsp-----AsnGlyAsnValLeuArgAlaIleGlu 401

Db 1231 GCGGGTACACCGGCTTCAACAGTGGCTTGTCAATGTAGA---CAGACTTATATCCA 1287  
Qy 402 PheProArgIleIysGlyIysProPheAsnIleAspThrAsp-----TrpPheAsn 419  
Db 1288 TTAAATCGTATCACTAGAGAAGCAGAAATTAACGTTGTGATAACGATAGCATGTGGCAAG 1347  
Qy 420 SerMetLeuSerGluIleGlyGlnPro 428  
Db 1348 ---CTTCTGTATTCACCAACCAACCA 1371

RESULT 6  
US-08-416-870C-5  
; Sequence 5. Application US/08416870C  
; Patent No. 5824862  
; GENERAL INFORMATION:  
; APPLICANT: HIYOSHI, TORU  
; APPLICANT: MINE, TOSHIKI  
; APPLICANT: KASAKURA, KEISUKE  
; APPLICANT: TYSON, ROBERT HUIW  
; APPLICANT: PAGE, ANTHONY MILLES JOHN  
; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE  
; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
; STREET: PO BOX 747  
; CITY: FALL CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/416, 870C  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 760-195P (PCT)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1624 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1409  
; US-08-416-870C-5

Alignment Scores:  
Pred. No.: 2,096-21 Length: 1624  
Score: 264.50 Matches: 109  
Percent Similarity: 40.54% Conservative: 56  
Best Local Similarity: 26.78% Mismatches: 173  
Query Match: 11.58% Indels: 69  
Gaps: 16

US-10-701-200-6 (1-437) x US-08-416-870C-5 (1-1624)

Qy 37 ILeuThrAlaGlyLeuAlaProCyLeuAsnSerAlaIleGlySerLeuIleGlu 56  
Db 222 ATTGTACATGTGAGAGACTGTGCGCTGACACTGTCTATTGAGGAATTTGTTGT 281

Qy 57 ArgIYrThrGluIleAspProSerIleGluIleIleCysTyArGlyIYrIYrIYrGly 76  
Db 282 GGCCTTAATATGATATATGCTGTACGTAGGATATGGAATTCAGGGTGGTATTAAGGT 341  
Qy 77 LeuLeuLeuGlyAspSerTyProValThrAlaGluValArgIYrIleGlyValLeu 96  
Db 342 TTCTATGCTTGTATACACCTTACCTTGAAGTCA-----AAGGTCTAAACGCAAT 392  
Qy 97 GlnArgPheGlyIYrSerValIleGlyAsnSerArgValIYrLeuThrAsnValIYrAsp 116  
Db 393 CACAAAGAGGCGTGAACCTGTCTTGGACATCAGCT----- 428  
Qy 117 CysValIYrAspGlyIYrLeuValIYrGluIYrGluAspProGluIYrValAlaIYrAspGln 136  
Db 429 -----GGAGGCCATGACCATGAAGATT-----GTTGACAC 461  
Qy 137 LeuValIYrAspGlyValAspIleLeuIleThrIleGlyIYrAspThrAsnThrAla 156  
Db 462 ATCCAGATCGTGTATTAATCAGCTTATGATTTGGTGTGATGCTCTCAAGAGGCT 521  
Qy 157 AlaIYrAspLeuAlaIYrPheLeuAlaArgAsnAsnTyGlyIYrLeuThrValIleGlyLeu 176  
Db 522 GCAGAGATATTTTGAAGAGATTAAGACGTGTCTCAAGTGTCTGTCTGTGCAATT 581  
Qy 177 ProIYrThrValAspAsnAspValPheProIleIYrGlnSerIYrAlaIYrThrAla 196  
Db 582 CCAAGACGATTAATATATATACAGATTAATGACATGATTTGGTATTCACACTGCA 641  
Qy 197 AlaGluGlnIYrAlaArgTyPheMetAsnValAlaIYrAsnAsnAlaAsnProArg 216  
Db 642 GTTGAAGAGCCCAACGTCCAAATAATGCTCATGTATGAAGCTGGAAGCCCGCAAT 701  
Qy 217 MetLeuIleValIleGluValMetGlyIYrArgAsnCysGlyIYrLeuThrAlaIYrAla 236  
Db 702 GGTATAGCGCTGTAAAGCTAATGAGTGCACACAGTGTATTATGCA----- 749  
Qy 237 GlnGluIYrArgIYrLeuLeuAspArgAlaGluIYrPheProGluIYrLeuThrArg 256  
Db 750 ---CACTATGCTACTGTGCGCAGCAGA----- 773  
Qy 257 GluSerTyGluValIleAlaValPheValProGluMetAlaIleAspLeuGluAlaGlu 276  
Db 774 -----GAGCTGATGTTGTTGATTCAGAGTCACTCTTCTATTCGAAGGTGA 824  
Qy 277 Ala-----LysArgLeuArgGluValMetAspIYrValAspCys 289  
Db 825 GGTGCGCTTTTATGATTTTGAAGAGCGTGAAGAGAAATGTCATATGTT----- 878  
Qy 290 ValAsnIlePheValSerGluIYrAlaGlyValGluAlaIleValAlaGluMetGlnAla 309  
Db 879 -----ATCGTTGTTGCGGAGGTCACAGGCGAAGAACTTATTATGAACAAAGATGA 932  
Qy 310 LysGlyGlnGluValProArgAspAlaPheGlyHis-----IleIYrLeuAspAlaValAsn 328  
Db 933 ATGGGG-----AAAGATCTTCAGCAATTCATTCCTTCTATGTT----- 974  
Qy 329 ProGlyIYrThrPheGlyIYrGluIYrPheAlaGluMetIleGlyIYrAlaGluIYrThrLeuVal 348  
Db 975 ---GGTCTTGTGTTATTCCAAAAGATTAAGAGACATTCACAGAAATCAAGACTACTATA 1031  
Qy 349 Gln-----LysSerGlyTyPheAlaIYrAlaIYrAlaSerAlaSerAsnValAspAsp 364  
Db 1032 AATTCAGATATATAGATCTTACATATCATGATTCGTGCAATTCCTTACATATCATGTGAC 1091  
Qy 365 MetArgLeuIleIYrSerCysAlaIYrPheValAlaValGluCysAlaPheArgArgIYrSer 384  
Db 1092 AATGTGTATTCACACTGTGTCACACAGAGGTGTTCATGAGGCCATGCGTGCATCACT 1151  
Qy 385 Gly-----ValIleGlyHisAspGluAspAsnGlyAsnValIYrLeuArgAlaIleGluPhePro 403  
Db 1152 GGTTCACACTGTGGC-----CAAGTAATATGTGCGCATATGC---TATATCCGTTTATAC 1202  
Qy 404 ArgIle-----LysGlyIYrIYrPheAsnIleAspThrAspIYrPheAsnSerMet 421



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Db      1203 AGCATCACAGAGGAGGACCAAGTTTCATTACTGATGAGATGTCGGGCAAGA---CTT 1259
Oy      422 LeuSerGluIleGlyInPro 428
Db      1260 CTCCTCTCAACCAACGACCA 1280

US-08-416-870C-1
Sequence 1, Application US/08416870C
Patent No. 5824862
GENERAL INFORMATION:
APPLICANT: HIYOSHI, TORU
APPLICANT: MINE, TOSHIKI
APPLICANT: KASAKA, KEISUKE
APPLICANT: TYSON, ROBERT HUW
APPLICANT: PAGE, ANTHONY MILES JOHN
TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR
TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALL CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416.870C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-195P (PCT)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 133..1587
US-08-416-870C-1

Alignment Scores:
Pred. No.: 5.7e-21 Length: 1978
Score: 262.00 Matches: 113
Percent Similarity: 38.41% Conservative: 56
Best Local Similarity: 25.68% Mismatches: 179
Query Match: 11.47% Indels: 92
DB: 1 Gaps: 17

US-10-701-200-6 (1-437) x US-08-416-870C-1 (1-1978)
Oy      7 TyrHisLeuThrAlaAspIleArgPheCysHisTrpPhePheLeuAsnPheAsnPheTyr 26
Db      388 TATTTCACTTCGAGATGATGTCGTCTGT----- 417
Oy      27 ThrIleMetAsnLysProLysValAlaIleLeuThrAlaGlyIleuAlaProCys 46
Db      418 -----ATGTAACTTGTGTGGTGTGTGTCCTGGG 447

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Oy	47	LeuSenSerAlaIleGlySerLeuIleGluArgYrThrGluIleAspProSerIleGlu	146
Db	448	CTTAACACAGCATCAGAGAGATTGTACATAGCTCCGATTTATGTATGAGTCAACAA	507
Oy	67	IleIleCysTrpArgGlyGlyTyrLeuGlyLeuLeuLeuGlyAspSerTyrProValThr	86
Db	508	GTCTTGGGTATCCATGGAGGCTTACAGGGGTTTCTATTCCAAAGATATCATCAATTGGCA	567
Oy	87	AlaGluValArgGlySerValaGlyValLeuGlnArgPheGlyGlySerValIleGlyAsn	106
Db	568	CCA-----AAGACTGTAAAGCATTCATTAACGGTGGGTACAAATCTTGGANCA	618
Oy	107	SerArgVallySerLeuThrAsnValLysAspCysValLysArgGlyLeuValLysGluGly	126
Db	619	TCACGA-----GAGGCG	630
Oy	127	GluAspProGlnLysValAlaAlaAspGlnLeuValLysAspGlyValAspIleLeuHis	146
Db	631	CATGATACCAAAAGATT---GTTGACAGCATACAGACCCGTAATTAATACAGTATAT	687
Oy	147	ThrIleGlyLysAspThrAsnThrAlaAlaAspLeuAlaAlaPheLeuAlaArg	166
Db	688	ATAATCGGTGTATGCACTCAGAAAGACACCTGTAATATATGAGAAATACAGCGG	747
Oy	167	AsnAsnTyrGlyLeuThrValIleGlyLeuProLysThrValAspAsnAspValPhePro	186
Db	748	CGTGCTCAAGTAATGTGTCTGGGATCCCAAGCAAACTGTATATGATATCCGTGT	807
Oy	187	IleLysGlnSerLeuGlyAlaTyrThrAlaAlaGlnGlnGlyAlaAspTyrPheMetAsn	206
Db	808	ATCAGCAAGTATTTGGTTTGTATACCTGCTTAAGAGGCTCAACGTGCCATTAATGCA	867
Oy	207	ValValAlaGluAsnAsnAlaAsnProArgMetLeuIleValHisGluValMetGlyArg	226
Db	868	GCTCATGTTGAAAGCGAAAGTCGGAATAATGTATGGTGGGGAAGCTAATGGCAGC	927
Oy	227	AsnCysGlyTyrPheThrAlaAlaThrAlaGlnGluTyrArgGlySerLeuLeuAspArgAla	246
Db	928	TATAGTGATTCATCGCA-----	945
Oy	247	GluThrPheLeuProGlnLeuGlyLeuThrArgGlnSerTyrGluValHisAlaValPheVal	266
Db	946	-----ATGTATGCCACTTTGGCGAGAGAGATGTGATCTCTGTTAAT	990
Oy	267	ProGluMetAlaIleAspLeuGluAlaGluAla-----LysArg	279
Db	991	CCAGAGTCACCCTTTATCTTGAAGAGATGTGTGACCTTTGAATCATTTGAAAAAGG	1055
Oy	280	LeuArgGluValMetAspLysValAspCysValAsnIlePheValSerGlyValaGly	299
Db	1051	CTCAAGAAATATGGGCATGCTT-----ATTGTGATAGCGGAAGAGCAGCGG	1098
Oy	300	ValGluAlaIleValAlaGlu--MetGlnAlaLysGlyGlnGluValProArgPheAla	318
Db	1099	CAAGAACTCTTTCAGAGAGAAATGCCGATCCAAAAAGCAACA-----GATGCT	1145
Oy	319	PheGlyHisIleLysLeuAspAlaValAsnProGlyLysTrpPheGlyGluGlnPheAla	338
Db	1150	TCGGGGAACAACTTCTCCAGAGATGTT---GGTTGTGGATTTCCCAAAATTCAGG	1203
Oy	339	GlnMetIleGlyAlaGluLysThrLeuValGln-----LysSerGly	352
Db	1204	GATCATTTT---GCTACAAATACTAAGATGCCATTACTTAAATATATGATCCGACT	1266
Oy	353	TyrPheAlaArgAlaSerAlaSerHisValAspAspMetArgLeuIleLysSerCysAla	372
Db	1261	TACATGATCTCGCTGTCTCAAGATATGCTCTGATAT-----GTATATTGCACT	1311
Oy	373	AspLeuAlaValGluCysAlaPheArgArgGlnSerGlyValIleGlyHisAspGluAsp	392
Db	1312	CTTCTGTGTCAAAGTTGTGTTCTACAGAGCAATGGCAGGCTCACAGGTTTCACTCCAGAA	1371

QY 393 -----AsnGlyAsnValLeuArgAlaIleGluPheProArgIleGlyGlyPro 410  
 Db 1372 CTTGTCATAGTCCG---CAGACTTATATACCATGATGATACCGAAGAAACAAAT 1428  
 QY 411 PheAsnIleAspThrAsp-----TrpPheAsnSerMetLeuSerGluIleGlyGlnPro 428  
 Db 1429 ATGGTGTTATATACATGACGAGATGTGGGACGT---CTTCTTTCGTCAACATCATGACCA 1485

RESULT 8  
 US-09-902-540-8974  
 ; Sequence 8974, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.  
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 8974  
 ; LENGTH: 1038  
 ; TYPE: DNA  
 ; ORGANISM: Myxococcus xanthus  
 US-09-902-540-8974

Alignment Scores:  
 Pred. No.: 2,726-21 Length: 1038  
 Score: 261.00 Matches: 96  
 Percent Similarity: 43.90% Conservative: 66  
 Best Local Similarity: 26.02% Mismatches: 141  
 Query Match: 11.43% Indels: 66  
 Gaps: 16

US-10-701-200-6 (1-437) x US-09-902-540-8974 (1-1038)

QY 34 LysValAlaIleLeuThrAlaGlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySer 53  
 Db 4 AAAGTCCCGCTGCTTACCGCGGGGTGACGTGCGCCGTGAACCCGTGATCCCGCC 63  
 QY 54 LeuIleGluArgTyrThrGluIleAspProSerIleGluIleCysTyrArgIleGly 73  
 Db 64 GTGTCGCGCGCCCAACGCC-----CACGCTTCGAGATGATGGCCCTCGAGATGCT 117  
 QY 74 TyrIleGlyLeuLeuLeuGlyAspSerTyrProValThrAlaGluValArgLysVala 93  
 Db 118 TGGAAAGGGTGTGTGAGACAACTTCGCTCACCGGTGAACCC-----ACGTCC 171  
 QY 94 GlyValIleuGlnArgPheGlyGlySerValIleGlyAsnSerArgVal-----Lys 110  
 Db 172 GGAATCTCCACCGG---GGCGAACCATCTCGGACCTCGGCGCTCAACCCGTTCAAG 228  
 QY 111 LeuThrAsnValIleAspCysValIleArgGlyLeuValIleGluGlyLysAspProGln 130  
 Db 229 GTCGAAACCGCGCTGAGCGCGTCAAGCGCGCC----- 261  
 QY 131 LysValAlaIleAspGlnLeuValIleAspGlyValAspIleuHsrThrIleGlyGly 150  
 Db 262 -----ATCGAAGCCCAACGCGCATCCACGCCCTCATCGCATTTGGTGGC 303  
 QY 151 AspAspThrAsnThrAlaAlaAlaAspLeuAlaIlePheLeuAlaArgAsnAsnTyrGly 170  
 Db 304 GAAGGCACTGCTGCGCCGCCACGCGCATG-----TCGCAAGAAAG 345  
 QY 171 LeuThrValIleGlyLeuProLysThrValAspAsnAspValPheProIleLysGlnSer 190  
 Db 346 CTCGCGATCGTGTGTGCGGAGAACCATCATGACAAAGCATCAACGCAACGCACTTCAC 405  
 QY 191 LeuGlyAlaIleThrAlaAlaGluGlnGlyAlaArgTyrPhe-----MetAsnVal 208

Db 406 TTCGCGTTGACACCGCGCGTCCGACATCCGACCGAGCCATTCGACCGCGTCCACC 465  
 QY 209 AlaGluAsnAlaAsnProArgMetLeuIleValIleGluValMetGlyArgAsnCys 228  
 Db 466 GCGGAGTCCGAC-----AAGCGGTCATCTGTCGAGAGTATGGGCGGTCACTG 516  
 QY 229 GlyThrPheThrAlaAlaThrAlaGlnIleuTyrArgLysLeuLeuAspArgIleGluTrp 248  
 Db 517 GCGTGAATTCGACC-----TACGGGGCATCGTGGCGGCGGAGC--- 558  
 QY 249 LeuProGluLeuGlyLeuThrArgLysSerTyrGluValIleAlaValPheValProGlu 268  
 Db 559 -----GTGATCTGTGTCGGAG 576  
 QY 269 MetAlaIleAspLeuGluAlaGluAlaValArgLeu-----ArgGluValMetAspLys 286  
 Db 577 ATTCGCGGACCTCGCGAAGGTGGCGGACATTCGACCGCGCGACCGGCGGCGCGC 636  
 QY 287 ValAspCysValAsnIlePheValSerGluGlyAlaGlyValGluAlaIleValAlaGlu 306  
 Db 637 ACCTTCTCCATT---GTGCTGTGGCGGAGGTACCGGCATCAAGCTGTGGCGGACAG 693  
 QY 307 MetGluAlaLysGlyGlnGluValProArgAspAlaPheGlyValIleLysLeuAspAla 326  
 Db 694 CAGAGACCTGTGTACACAGCGCGCATCGACGAGCGAGCGCGCGCTCGGTGGC 753  
 QY 327 ValAsnProGlyLysThrPheGlyGluGlnPheAlaGlnMetIleGlyAlaGluTyrThr 346  
 Db 754 GTG-----GGCACCATCTGGCGGACGAAATCGAGCGCGCACGCGCTTCAG---ACG 804  
 QY 347 LeuValGlnLysSerGlyTyrPheAlaArgAlaSerAlaSerAsnValAspMetArg 366  
 Db 805 CGCGTGTCCGTGCTGGCCCATTCGACGCGCGCGCGCGCGCGCATGACCGCGTGC 864  
 QY 367 Leu-----IleLysSerCysAlaAspLeuAlaValGluCysAlaPheArg 381  
 Db 865 CTCGCCACCCGCTACGGCGGTCCACGCTGC---GACATGTGCGCGCGCGGAGTTCCGG 921

RESULT 9

US-09-902-540-958/c  
 ; Sequence 958, Application US/09902540  
 ; Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 958

LENGTH: 10391

TYPE: DNA

ORGANISM: Myxococcus xanthus

US-09-902-540-958

Alignment Scores:

Pred. No.: 1,036-19 Length: 10391  
 Score: 261.00 Matches: 96  
 Percent Similarity: 43.90% Conservative: 66  
 Best Local Similarity: 26.02% Mismatches: 141  
 Query Match: 11.43% Indels: 66  
 Gaps: 16

US-10-701-200-6 (1-437) x US-09-902-540-958 (1-10391)

Qy 34 LyeValAlaIleuThrAlaGlyLeuAlaProCysLeuAsnSerAlaIleGlySer 53  
Db 3602 AAGTCCCTGCTGCTGACCGGGGGTGAATGCTCCCGCTGAACGGCTCATCCGGCC 3543

Qy 54 LeuIleGluArgTyrThrGluIleAspProSerIleGluIleIleCysTyrArgGly 73  
Db 3542 GTCGTCGGCGCCGCAACGCC-----CACGGCTTCAGATGATGAGGCTCCGAGATGGT 3489

Qy 74 TyrLysGlyLeuLeuLeuGlyAspSerTyrProValThrAlaGluValArgLysAla 93  
Db 3488 TGAAGGGGTGTGGAGGACACACCTCCGCTCAAGGTGAAC-----ACGTCC 3435

Qy 94 GlyValLeuGlnArgPheGlyGlySerValIleGlyAsnSerArgVal-----Lys 110  
Db 3434 GGAATCTTCACCGG---GGCGAACCATCTCGGCACTTCGCGCGTCAACCGCTTCAAG 3378

Qy 111 LeuThrAsnValLysAspCysValLysArgGlyLeuValLysGluGlyAspProGln 130  
Db 3377 GTCGAAACGGGCTGAGCGCGTCACAGCGCC----- 3345

Qy 131 LysValAlaAlaAspGlnLeuValLysAspGlyValAspIleLeuHISThrIleGly 150  
Db 3344 -----ATCGAACGCAACGGCGCATCCACCGCTCATCGCATTCGCTGGTGC 3303

Qy 151 AspAspThrAsnThrAlaAlaAspLeuAlaAlaPheLeuAlaArgAsnAsnTyrGly 170  
Db 3302 GAAGGCAACGCTGCTGCGCCGCGCACCGCATG-----TGCAGGAAGA 3261

Qy 171 LeuThrValIleGlyLeuProLysThrValAspAsnAspValPheProIleLysGlnSer 190  
Db 3260 CTGCGCATGCTGCGGTGCGGAGACCATCGACACATCAACGCGCAGCATTCAC 3201

Qy 191 LeuGlyAlaThrThrAlaAlaGluGlnGlyAlaArgTyrPhe-----MetAsnValVal 208  
Db 3200 TTCGGCTTCACACGGCGCTGCCCATCGCACCGGCGCATTCGACTCCACC 3141

Qy 209 AlaGluAsnAsnAlaAsnProArgMetLeuIleValIleGluValMetGlyArgAsnCys 228  
Db 3140 GCGGAGTCCGAC-----AACCGCTCATCTGCGAGGTGATGGCGCTCACGTG 3090

Qy 229 GlyTyrLeuThrAlaAlaThrAlaGlnGluTyrArgLysLeuLeuAspArgAlaGluTyr 248  
Db 3089 GGCCTGATTCGAC-----TAGCGGGCATCGCTGGCGCGCGGAC--- 3048

Qy 249 LeuProGluLeuGlyLeuThrArgGluSerTyrGluValHISAlaValPheValProGlu 268  
Db 3047 -----GTCATCTGCTGCCGAG 3030

Qy 269 MetAlaIleAspLeuGluAlaGluAlaLysArgLeu-----ArgGluValMetAspLys 286  
Db 3029 ATTCCGCCCACTCTCGGAAGGTGGCGAGACATTCACGCGCGCCACGCGGGCGGGCGC 2970

Qy 287 ValAspCysValAsnIlePheValSerGluGlyValGluValAlaIleValAlaGlu 306  
Db 2969 ACCCTTCCATT---GTCGTGTGGCGAGGTGCGGACATCAAGCTGTGGCGGACAG 2913

Qy 307 MetGlnAlaLysGlyGlnGluValProArgAspAlaPheGlyHISLysLeuAspAla 326  
Db 2912 CAGGAGCAGCTGTCACACGCGGCACTGACGACGAGGCGCGCGCTCGTGGC 2853

Qy 327 ValAsnProGlyLysTyrPheGlyGluGlnPheAlaGlnMetIleGlyAlaGluLysThr 346  
Db 2852 GTG-----GGCACCATCTGGCGCACGAAATCGAGCGGCGACCGGCTTCGAG---ACG 2802

Qy 347 LeuValGlnLysSerGlyTyrPheAlaArgAlaSerAlaSerAsnValAspAspMetArg 366  
Db 2801 CGGCTGTCGAGTGGCGCACATCCACGCGCGCGCGCCACCGGCGATGACCGGTG 2742

Qy 367 Leu-----IleLysSerCysAlaAspLeuAlaValGluCysAlaPheArg 381  
Db 2741 CTGCGCCACCGCTACGCGCTCCAGCTGC---GACATGTGTGGCGCGCGGAGTTCCGG 2685

Qy 382 ArgGluSerGlyValIleGlyHISAsp 390  
Db 2684 AAGATGCCCGCGCTGGAGGCAACGAC 2658

RESULT 10  
US-08-416-870C-9  
Sequence 9, Application US/08416870C  
Patent No. 5824862  
GENERAL INFORMATION:  
APPLICANT: HIYOSHI, TORU  
APPLICANT: MINE, TOSHIKI  
APPLICANT: KASANO, KEISUKE  
APPLICANT: TYSON, ROBERT HUW  
APPLICANT: PAGE, ANTHONY MILES JOHN  
TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE  
TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR  
TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
STREET: PO BOX 747  
CITY: FALL CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/416,870C  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 760-195P(PCT)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1558 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1278  
US-08-416-870C-9

Alignment Scores:  
Pred. No.: 6,8e-21 Length: 1558  
Score: 260.00 Matches: 107  
Percent Similarity: 41.15% Conservative: 65  
Best Local Similarity: 25.60% Mismatches: 174  
Query Match: 11.38% Indels: 72  
Gaps: 16

US-10-701-200-6 (1-437) x US-08-416-870C-9 (1-1558)

Qy 37 IleLeuThrAlaGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGlu 56  
Db 148 ATTGTTACATGTGTGCTGCTGCTGCTCAAGGCTTAATCTCATCAAGAAATCGTTGT 207

Qy 57 ArgTyrThrGluLeuAspProSerIleGluIleIleCysTyrArgGlyGlyTyrLysGly 76  
Db 208 GGAATGCTTACATGATGTGTGCAAGAAATCTTCGCGCATTCAGAGGAGTTACAGAGC 267

Qy 77 LeuLeuLeuGlyAspSerTyrProValThrAlaGluValArgLysAlaGlyValLeu 96





Db 1443 GCGGTGTGGGCTCGCGGAGCGCTGCGGACCTGCTGCGCCGACACATC 1384  
Qy 313 -----GluValProArgAspAlaPheGlyHisIleLys----- 323  
Db 1383 GAGCGGAGATTGGCTGACGCGTGTGGGACCTCCAGCGGGGGGACCCCAAGCGG 1324  
Qy 324 -----LeuAspAlaValAsnProGly 330  
Db 1323 GCGGACGGGTACTGCGCACTCGCTACGCTGCAAGGTGCTGAGCTGTGAGCGGGG 1264  
Qy 331 LysTyr 332  
Db 1263 CAGTGG 1258

RESULT 13  
US-08-956-171E-312  
Sequence 312, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956, 171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7972 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-956-171E-312  
SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Alignment Scores:  
Pred. No.: 6.18e-16 Length: 7972  
Score: 228.00 Matches: 102  
Percent Similarity: 42.24% Conservative: 75  
Best Local Similarity: 24.34% Mismatches: 147  
Query Match: 9.98% Indels: 95  
DB: 4 Gaps: 19

US-10-701-200-6 (1-437) x US-08-956-171E-312 (1-7972)  
Qy 26 TyrThrLeuMetAsnLysProLysValAlaIleLeuThrAlaGlyLysLeuAlaPro 45  
Db 3647 TATGTGTCATG-----AAGAAATATGCAGTTTAACTTACGTGTGAGTACCT 3697  
Qy 46 CysLeuAsnSerAlaIleLysSerLeuIleGluArgTyrThrGluIleAspProSerIle 65  
Db 3698 GGAATGAATGTCGCGTAGACAGCATGTGCT-----ACAGCAATTTAAATGAATAAT 3751  
Qy 66 GluIleIleCysTyrArgGlyLysValLeuLeuLeuGlyAspSerTyrProVal 85  
Db 3752 GAAGTTATGCTGTGTATCATGTTTCCAGAGATTCTTAAATGATATTTCAATCACTT 3811  
Qy 86 ThrAlaGluValArgLysLysAlaGlyValLeuGlnArgPheGlyLysValIleGly 105  
Db 3812 -----GAATTAGATTCAGTGGGATGAGTACGATTCAGCGT---GAGAGTACATTTCTGTAT 3862  
Qy 106 AsnSerArgValLysLeuThrAsnValLysAspCysValLysArgGlyLeuValLysGlu 125  
Db 3863 TCAGCAGA-----TGCCAGAG-----TTTAAAGAG 3889  
Qy 126 GlyGluAspProGlnLysValAlaAlaAspGlnLeuValLysAspGlyValAspIleLeu 145  
Db 3890 ---CAAGAACTACGTAAAGTTCCAACTTACGTAAAGAGGAGATTGAGGCTT 3946  
Qy 146 HisThrIleGlyLysAspThrAsnThrAlaAlaAlaAspLeuAlaAlaPheLeuAla 165  
Db 3947 GTAGTTATGTGTGTGACCGTAGTATCGCGGTACCAAGCATGAGATGAGAAATGTAA 4006  
Qy 166 ArgAsnAsnTyrGlyLeuThrValIleGlyLeuProLysThrValAspAsnAspValPhe 185  
Db 4007 GAA-----ATTCAACTATCGGTATTCCTGTGATGACATGACATGATATCAAT 4054  
Qy 186 ProIleLysGlnSerLeuGlyValAspThrAlaAlaGluGlnGlyAlaArgTyrPheMet 205  
Db 4055 GGTACTGATTTTACATTTGATTTGACACAGCATTTAAATCAATTTGGCTTATGCGAC 4114  
Qy 206 AsnValValAlaGluAsnAsnAlaAsnProArgMetLeuIleValHisGluValMetGly 225  
Db 4115 AAAATTAGATGATACGTGCGTCAAGTCACGACGACAACTTATCATTT---GAGCAATGGGC 4171  
Qy 226 ArgAsnCysGlyTyrLeuThrAlaAlaThrAlaGlnGluTyrArgLysLeuLeuAspArg 245  
Db 4172 CGTGAATTGG-----GATCTTA 4189  
Qy 246 AlaGluTyrLeuProGluLeuGlyLeuThrArgLysSerTyrGluValHisAlaValPhe 265  
Db 4190 GCAATTATG-----GCTGATTA-----TCAGTTGGTCTGACGACATTTGA 4231  
Qy 266 ValProGluMetAlaIleAspLeuGluAlaGluAlaLysArgLeuArgGluValMetAsp 285  
Db 4232 GTTCCAGAAAGTAAAAACGAT-----ATTAAAGAAATATAGTGAT 4270  
Qy 286 LysValAspCysValAsnIlePheValSerGluGlyAlaGlyValGlu----- 301  
Db 4271 AAAATTGAA-----CAAGTATTTAAAGGTGTAGAA 4303  
Qy 302 -----AlaIleValAlaGluMetGlnAlaLysGlyGlnGluValProArgAspAla 318  
Db 4304 CACTCAATGCTTCTGTACAGAGAGGTGTATGACTGCGCAAGATTTGAAAAAGATTA 4363  
Qy 319 PheAlaGlnMetIleGlyAlaGluLysThrLeuValGlnLysSerGlyTyrPheAlaArg 356  
Db 4364 TCACATATCATCAATGTTGAT-----AATAGAGTGTGTGTAGTACGCTCAACGT 4417  
Qy 337 PheAlaGlnMetIleGlyAlaGluLysThrLeuValGlnLysSerGlyTyrPheAlaArg 356  
Db 4418 GGTGTAGCCCAACAGGTGCGATAGATTAGATCACTGTTAGTGTGATATGCG--- 4474  
Qy 357 AlaSerAlaSerAsnValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaVal 376  
Db 4475 -----GTAGACTTATTAATG 4489

QY 377 GluCysAlaPheArgGluSerGlyValIleGlyHisAspGluAspAsnVal 396  
Db 4490 CAAGGTGAACAGCTAAGGGTGTGAAT-----AAGAACAAATAAA 4531  
QY 397 LeuArgAlaIleGluPheProArgIleValGlyLysProPheAsnIleAspThrAsp 416  
Db 4532 ATGTGCAACATCTTTGATGAATTTTGTGATGAAGATCAATAATTTGATTAAGT 4591  
QY 417 -TrpPheAsnSerMetLeuSerGluIleGlyInProGlyGlyLysValGlu 434  
Db 4592 CTATATGAACTTGCTAACAAGATTATATTAAGATTTCAGAGGAATTTATAAA 4646  
RESULT 14  
US-08-781-986A-312  
Sequence 312, Application US/08781986A  
Patent No. 6737248  
GENERAL INFORMATION:  
APPLICANT: Charilee Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 312:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7972 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-312  
Alignment Scores:  
Prod. No.: 6.18e-16 Length: 7972  
Score: 228.00 Matches: 102  
Percent Similarity: 42.24% Conservative: 75  
Best Local Similarity: 24.34% Mismatches: 147  
Query Match: 9.38% Indels: 95  
Gaps: 19  
US-10-701-200-6 (1-437) x US-08-781-986A-312 (1-7972)  
QY 26 TyrThrLeuMetAsnLysProLysValAlaIleLeuThrAlaGlyGlyLeuAlaPro 45  
Db 3647 TATGTGCTGATC-----AAGAAATATGCAAGTTTAACTAGTGATGAGATTCACT 3697  
QY 46 CysLeuAsnSerAlaIleGlySerLeuIleGluArgTyrThrGluIleAspProSerIle 65  
Db 3698 GGAATGAATGCTCCGTAAGACAGTTTCTGCT-----ACAGCAATTTCAATGAATTT 3751

QY 66 GluIleIleCysTyrArgGlyGlyTyrLysGlyLeuLeuLeuGlyAspSerTyrProVal 85  
Db 3752 GAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3811  
QY 86 ThrAlaGluValArgLysValAlaGlyValLeuGluArgPheGlyGlySerValIleGly 105  
Db 3812 -----GAATTAGATCAAGTGGGATGACATTCACCGT---GGAGATCAATCTTGAT 3862  
QY 106 AsnSerArgValLysLeuThrAsnValLysAspCysValLysArgLysLeuValLysGlu 125  
Db 3863 TCAGCAAGA-----TGCCACAG-----TTAAGAG 3889  
QY 126 GlyGluAspProGluLysValAlaAlaAspGluLeuValLysAspGlyValAspIleLeu 145  
Db 3890 ---CAAGAGTACATAAGTTGCAATCGAAACTTGTGTAAGAGGATGAGGCGCTT 3946  
QY 146 HisThrIleGlyGlyAspAspThrAsnThrAlaAlaAspLeuAlaAlaPheLeuAla 165  
Db 3947 GTAGTTATGTTGTGTCACGATGATTCGCGGTGCAACGATCAGTCAAGATGTAA 4006  
QY 166 ArgAsnAsnTyrGlyLeuThrValIleGlyLeuProLysThrValAspAsnAspValPhe 185  
Db 4007 GAA-----ATTCAACTATCGGTATTCCTGTCGTCGATGACATGATATCAAT 4054  
QY 186 ProIleLysGlnSerLeuGlyAlaTyrThrAlaAlaGluGlnGlyAlaArgTyrPheMet 205  
Db 4055 GGTACTGATTTTACATTTGATTTGACACAGCATTAATGATTAATGCTTAAGTCAC 4114  
QY 206 AsnValValAlaGluAsnAsnAlaAsnProLysMetLeuIleValHisGluValMetGly 225  
Db 4115 AAATTAGAGATCTCGCTCAAGTCAAGCAGCAACATTTATCACT---GAAGCAATGGGC 4171  
QY 226 ArgAsnCysGlyTyrPheThrAlaAlaThrAlaGlnGluTyrArgLysLeuAspArg 245  
Db 4172 CGTGATTTGGA-----GATCTA 4189  
QY 246 AlaGluTyrPheProGluLeuGlyLeuThrArgGluSerTyrGluValHisAlaValPhe 265  
Db 4190 GCATTTATG-----GCTGATTA-----TCAGTTGCTGTCAGCAATGTA 4231  
QY 266 ValProGluMetAlaIleAspLeuGluAlaGluAlaLysArgLeuArgGluValMetAsp 285  
Db 4232 GTTCCAGAGTGAACAGAT-----ATTAAAGAAATAGCTGAT 4270  
QY 286 LysValAspCysValAsnIlePheValSerGluGlyAlaGlyValGlu----- 301  
Db 4271 AAAATTGAA-----CAAGTATTTAAACGTGTAAAGAA 4303  
QY 302 -----AlaIleValAlaGluMetGlnAlaLysGlyGlnGluValProArgAspAla 318  
Db 4304 CACTCAATCGTTCTTGTAGCAGAGAGTTGATGATCCTGCCAGATTTGTCAAAAAGAAATTA 4363  
QY 319 PheGlyHisIleLysLeuAspAlaValAsnProGlyLysTyrPheGly-----GluGln 336  
Db 4364 TCACAATATCATCAATGTGAT-----AATAGAGTGTCTGTAGTCACTGTTCAACGT 4417  
QY 337 PheAlaGluMetIleGlyAlaGluLysThrLeuValGlnLysSerGlyTyrPheAlaArg 356  
Db 4418 GGTGTGAGCCCAACAGGTGCGATGAAGTTTATGATCACTCACTTTAGGTGATGCG--- 4474  
QY 357 AlaSerAlaSerAsnValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaVal 376  
Db 4475 -----GTAGACTTATTAATG 4489  
QY 377 GluCysAlaPheArgGluSerGlyValIleGlyHisAspGluAspAsnVal 396  
Db 4490 CAAGGTGAACAGCTAAGGGTGTGAAT-----AAGAACAAATAAA 4531  
QY 397 LeuArgAlaIleGluPheProArgIleValGlyLysProPheAsnIleAspThrAsp 416  
Db 4532 ATGTGCAACATCTTTGATGAATTTTGTGATGAAGATCAATAATTTGATTAAGT 4591  
QY 417 -TrpPheAsnSerMetLeuSerGluIleGlyInProGlyGlyLysValGlu 434

Db 4592 CTATATGAACCTGCTACACAGTATCTATATTAAGATTTCAGAGGAATTTATATAA 4646

RESULT 15  
US-09-489-039A-5087  
Sequence 5087, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709 2004001  
CURRENT APPLICATION NUMBER: US/09/489, 039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 5087  
LENGTH: 1017  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5087

Alignment Scores:  
Pred. No.: 3,16e-17 Length: 1017  
Score: 227.00 Matches: 105  
Percent Similarity: 38.84% Conservative: 62  
Best Local Similarity: 24.42% Mismatches: 136  
Query Match: 9.94% Indels: 128  
DB: 4 Gaps: 18

US-10-701-200-6 (1-437) x US-09-489-039A-5087 (1-1017)

QY 13 ILeArgPhcYshIstRphPheLeuAenPheAsnPhetYrThreUmetAenLysPro 32  
Db 22 ATTATTTTTC-----TTCCTAAGTTCAGAGTACTCATGTT----- 60  
QY 33 LysLysValAlaIleLeuThrAlaGlyGlyLeuAlaProCysLeuAenSerAlaIleGly 52  
Db 61 AAGAAATATCGTGTGTGTGACACAGTGGCGGTGATGCCCGGCGCATGAAACGACGATTCGT 120  
QY 53 SerLeuIleGluArgYrThrGluIleAspProSerIleGluIleIleCysYrArgGly 72  
Db 121 GCGGTGTGGCC-----GCGCATTTAACGGAAGTCTGGAGTTTGGATCTATGAC 174  
QY 73 GlyTyrLysGlyLeu-----LeuLeuGlyAspSerYrProValThrAla 87  
Db 175 GGTTACTCTCGGATTGTATGAAGACCGATGCTTCACTGACCGTTTACGCGTTTCCGAC 234  
QY 88 GluValArgLysLysAlaGlyValLeuGlnArgPheGlyGlySerValIleGlyAenSer 107  
Db 235 ATGATCAACCGC-----GGCGTACCTTCTCGGCGCTCCGCT 270  
QY 108 ArgValLysLeuThrAenValLysAspCysValLysArgGlyLeuValLysGluGly 127  
Db 271 CGC-----TTCGCGGAATTCGCGAA-----GAA 294  
QY 128 AspProGlnLysValAlaAlaAspGlnLeuValLysAspGlyValAspIleLeuHleThr 147  
Db 295 CACATCCGCGCTGTGCTATCGAAACAAACAAAGACCGCGCTGACGCGCTGTGGTT 354  
QY 148 IleGlyLysAspAspThrAenThrAlaAlaAlaAspLeuAlaAlaPheLeuAlaArgAen 167  
Db 355 ATCGGCGGTGACGGTTCCTATATGGGCGGATGCGCCTG-----ACC 396  
QY 168 AsnTyrGlyLeuThrValIleGlyLeuProLysThrValAspAsnAspValPheProIle 187  
Db 397 GAGATGGCTTCCTCATGATCGGCTGCGGACCATCGACAAACATATCAAGGCACT 456  
QY 188 LysGlnSerLeuGlyValArgThrAlaAlaGluGlnGlyValArgYrPheMetAenVal 207  
Db 457 GACTACACCATCGGCTTCTTACTGCGCTGAGCACCGTGTGGAAGCATGACCGTTTG 516

QY 208 ValAlaGluAsnAsnAlaAsnProArgMetLeuIleValHisGluValMetGlyArgAen 227  
Db 517 CGGACACCTCTCTTCGACACGATCTCCGGTG--GAAGTGAATGGCCCTTAC 573  
QY 228 CysGlyTyrPheThrAlaAlaThrAlaGlnGluYrArgLysLeuAspArgAlaGlu 247  
Db 574 TTGGGACCTTACCTTGGCGGCGG-----ATTCCGCGGCTGTAG 618  
QY 248 TrpLeu-----ProGluLeuGlyLeuThrArgGluSerYrGluValHisAlaValPhe 265  
Db 619 TTCATCATGCTCTCGAAGTGAATATACCCGTAC----- 654  
QY 266 ValProGluMetAlaIleAspLeuGluAlaGluAlaLys----- 278  
Db 655 -----GATCTGTGTGGAGAAATCAAGCCGATTCGCGAAAGGAAA 696  
QY 279 -----ArgLeuArgGluValMetAspLysValAspCysValAsnIlePhe 293  
Db 697 AAACACGCTATCTGTGGCCATCACCGACATGTGCGACGTTGACAGCTGGCAACTAC 756  
QY 294 ValSerGluGlyAlaGlyValGlu-----AlaIleValAlaGluMetGlnAlaLys 310  
Db 757 ATCGAAGAAAGACATGCGCGTGAACCTGCGCCACCGTCTCGGCACATTCAGCGCGGC 816  
QY 311 GlyGlnGluValProArgPheAlaPheGlyHisIleLysLeuAspAlaValAsnProGly 330  
Db 817 GGTTCCTCCGCTTCTTACGAC----- 837  
QY 331 LysTrpPheGlyGluGlnPheAlaGlnMetIleGlyAlaGluLysThrLeuValGlnLys 350  
Db 837 ----- 837  
QY 351 SerGlyTyrPheAlaArgAlaSerAlaSerAenValAsp-AspMetArgLeuIleLysSe 370  
Db 838 -----CGCATCTGGCTTCCCGCATGCGCGGCGCTATGAGCTGTG 882  
QY 370 rCysAlaAspLeuAlaValGluCysAlaPheArgArgGluSerGlyValIleGlyHisAs 390  
Db 883 CTGCGAGGCGCATGGCGGC-CGTGTGCTGCGCATCGAAGCGAAGCTGTGCACACGCA 941  
QY 390 pGluAspAsnGlyAenValLeuArgAlaIleGluPheProArgIleLysGlyLysPr 410  
Db 942 C-----ATCATGATGCCATCGAAGCAATGAAG-----CGTCC 974  
QY 410 oPheAsnIleAspThrAspTrpPheAsn 419  
Db 975 GTTCAAG-----AACGACTGCGTGAAT 996

Search completed: March 31, 2005, 10:31:57  
Job time : 263 secs



GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: March 31, 2005, 09:54:39 ; Search time 55 Seconds  
(without alignments)  
593.121 Million cell updates/sec

Title: US-10-701-200-6  
Perfect score: 2284  
Sequence: 1 DVTWPHYLTRDIRFCHMFP.....FNSMLSEIGQPKGKVEVSH 437

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2284	100.0	437	US-09-934-901-16	Sequence 16, Appl
2	2284	100.0	437	US-09-934-868-6	Sequence 6, Appl
3	2284	100.0	437	US-10-321-210-16	Sequence 16, Appl
4	2284	100.0	437	US-10-320-874-16	Sequence 16, Appl
5	270	11.8	483	US-08-416-870C-4	Sequence 4, Appl
6	264.5	11.6	469	US-08-416-870C-6	Sequence 6, Appl
7	262	11.5	485	US-08-416-870C-2	Sequence 2, Appl
8	261	11.4	345	US-09-902-540-16136	Sequence 16136, A
9	260	11.4	426	US-08-416-870C-10	Sequence 10, Appl
10	227	9.9	338	US-09-489-039A-12258	Sequence 12258, A
11	226.5	9.9	345	US-09-134-001C-3774	Sequence 3774, Ap
12	220	9.6	330	US-09-543-681A-8337	Sequence 8337, Ap
13	220	9.6	335	US-09-583-110-5099	Sequence 5099, Ap
14	218.5	9.6	321	US-09-134-000C-5332	Sequence 5332, Ap
15	215.5	9.4	323	US-09-107-532A-6470	Sequence 6470, Ap
16	211.5	9.3	522	US-08-416-870C-8	Sequence 8, Appl
17	210	9.2	389	US-09-949-016-9488	Sequence 9488, Ap
18	206.5	9.0	781	US-08-280-690-2	Sequence 2, Appl
19	204.5	9.0	784	US-09-949-016-6251	Sequence 6251, Ap
20	201.5	8.8	798	US-09-949-016-11096	Sequence 11096, A
21	201	8.8	343	US-09-887-054-2	Sequence 2, Appl
22	182	8.0	307	US-09-710-279-2122	Sequence 2122, Ap
23	181	7.9	550	US-09-198-452A-225	Sequence 225, Ap
24	181	7.9	556	US-09-438-185A-210	Sequence 210, App
25	179	7.8	556	US-09-438-185A-162	Sequence 162, App
26	171.5	7.5	544	US-09-198-452A-180	Sequence 180, App
27	148	6.5	696	US-09-949-016-8015	Sequence 8015, App

28	120	5.3	169	4	US-09-107-433-2681	Sequence 2681, Ap
29	113.5	5.0	845	4	US-09-198-452A-458	Sequence 458, App
30	113.5	5.0	847	4	US-09-438-185A-439	Sequence 439, App
31	107	4.7	810	4	US-09-583-110-4352	Sequence 4352, Ap
32	107	4.7	816	4	US-09-107-433-4504	Sequence 4504, Ap
33	106.5	4.7	543	4	US-09-248-796A-17070	Sequence 17070, A
34	101.5	4.4	1427	4	US-09-538-092-1044	Sequence 1044, Ap
35	100.5	4.4	341	4	US-09-248-796A-17051	Sequence 17051, A
36	99.5	4.4	742	4	US-09-489-039A-7998	Sequence 7998, Ap
37	99.5	4.4	1038	3	US-09-541-782-4	Sequence 4, Appl
38	99.5	4.4	1038	4	US-09-723-820-4	Sequence 4, Appl
39	99.5	4.4	1038	4	US-10-270-085-4	Sequence 4, Appl
40	97.5	4.3	413	4	US-09-603-208A-8	Sequence 8, Appl
41	97.5	4.3	538	4	US-09-603-208A-6	Sequence 6, Appl
42	97.5	4.3	724	4	US-09-489-039A-12100	Sequence 12100, A
43	96.5	4.2	458	4	US-09-489-039A-9184	Sequence 9184, Ap
44	96	4.2	863	4	US-09-328-352-6730	Sequence 6730, Ap
45	95.5	4.2	412	4	US-09-252-991A-30252	Sequence 30252, A

## ALIGNMENTS

RESULT 1  
US-09-934-901-16  
Sequence 16, Application US/09934901  
Patent No. 6555353  
GENERAL INFORMATION:  
APPLICANT: Koffas, Matheos  
APPLICANT: Odom, J. Martin  
APPLICANT: No. 6555353ton, Kelley C.  
APPLICANT: Ye, Rick  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/09/934,901  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,906  
PRIOR FILING DATE: September 1, 2000  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 16  
LENGTH: 437  
TYPE: PRT  
ORGANISM: METHYLOMONAS SP.  
US-09-934-901-16

Query Match	100.0%;	Score 2284;	DB 4;	Length 437;
Best Local Similarity	100.0%;	Pred. No. 1.6e-215;		
Matches 437;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DVTWPHYLTRDIRFCHMFP	LNFPYTLNWKPKKVA	ILITAGLAPCLNSAIGSLIBRYTE 60
DB	1	DVTWPHYLTRDIRFCHMFP	LNFPYTLNWKPKKVA	ILITAGLAPCLNSAIGSLIBRYTE 60
QY	61	IDPSIEILICRGYKGLLD	SYPTVAEYKKAQV	LQRFSGSVIGNSRVKLTINVKCVKR 120
DB	61	IDPSIEILICRGYKGLLD	SYPTVAEYKKAQV	LQRFSGSVIGNSRVKLTINVKCVKR 120
QY	121	GLYKEGDPKVAADQ	LKQGVILITIGDD	NTNTAAADLAFLARNNGVLTITGPKTV 180
DB	121	GLYKEGDPKVAADQ	LKQGVILITIGDD	NTNTAAADLAFLARNNGVLTITGPKTV 180
QY	181	DNDVFPKQSLGAMTA	EGGARFEMNVVAENNN	PNMLIYHEVMGRNGCLTAAAOEYR 240
DB	181	DNDVFPKQSLGAMTA	EGGARFEMNVVAENNN	PNMLIYHEVMGRNGCLTAAAOEYR 240
QY	241	KLIDRAEWLPBELG	LTRESYEVHAFVPEMA	IDLEAKRLREYVDVNVIVSBCAGV 300
DB	241	KLIDRAEWLPBELG	LTRESYEVHAFVPEMA	IDLEAKRLREYVDVNVIVSBCAGV 300
QY	301	EATVAEMQAGQVPR	DAFGHITKLDVNPCKM	GEQFOAOTIGAEKTLVQKSGYFARASAS 360
DB	301	EATVAEMQAGQVPR	DAFGHITKLDVNPCKM	GEQFOAOTIGAEKTLVQKSGYFARASAS 360

QY 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
QY 421 MLSEIGOPKGGKVEVSH 437  
DB 421 MLSEIGOPKGGKVEVSH 437

## RESULT 2

US-09-934-868-6  
Sequence 6, Application US/09934868  
Patent No. 6689601  
GENERAL INFORMATION:  
APPLICANT: Koffas, Matheos  
APPLICANT: Odom, James M  
APPLICANT: Schenzle, Andreas J  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL156 US NA  
CURRENT APPLICATION NUMBER: US/09/934, 868  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229, 858  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 6  
LENGTH: 437  
TYPE: PR1  
ORGANISM: METHYLIOMONAS SP.  
US-09-934-868-6

Query Match 100.0%; Score 2284; DB 4; Length 437;  
Best Local Similarity 100.0%; Pred. No. 1,6e-215;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHYLTADIRFCHEWFLNFYTLNKKPKVAIITAGGLAPCLNSAIGSLIERYTE 60  
DB 1 DVVTWPHYLTADIRFCHEWFLNFYTLNKKPKVAIITAGGLAPCLNSAIGSLIERYTE 60  
QY 61 IDPSIEIICRGYKGLLDGSDYPTAEVRKKAQVLOFGSGVIGNSRVKLTNVKDCVR 120  
DB 61 IDPSIEIICRGYKGLLDGSDYPTAEVRKKAQVLOFGSGVIGNSRVKLTNVKDCVR 120  
QY 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLARNNYGLTVIGL.PKTV 180  
DB 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLARNNYGLTVIGL.PKTV 180  
QY 181 DNDVFPKISLGAWTAABEGARFEMNVVAENNANPRMLIVHEVMGRNCGLTAATQOYR 240  
DB 181 DNDVFPKISLGAWTAABEGARFEMNVVAENNANPRMLIVHEVMGRNCGLTAATQOYR 240  
QY 241 KLLDRAEWLPELGLTRSEYEVHAFVPEMAIDLEBAKRLREVMKVCVNI.FVSEGAGV 300  
DB 241 KLLDRAEWLPELGLTRSEYEVHAFVPEMAIDLEBAKRLREVMKVCVNI.FVSEGAGV 300  
QY 301 EAIIVAMQAKGQEVPRDAFGHILKDAVNPCKWFGQFQMGIGAEKTLVOKSGVFAPASAS 360  
DB 301 EAIIVAMQAKGQEVPRDAFGHILKDAVNPCKWFGQFQMGIGAEKTLVOKSGVFAPASAS 360  
QY 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
QY 421 MLSEIGOPKGGKVEVSH 437  
DB 421 MLSEIGOPKGGKVEVSH 437

## RESULT 3

US-10-321-210-16  
Sequence 16, Application US/10321210  
Patent No. 6767744

GENERAL INFORMATION:  
APPLICANT: Koffas, Matheos  
APPLICANT: Odom, J. Martin  
APPLICANT: No. 6767744ton, Kelley C.  
APPLICANT: Ye, Rick  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/10/321, 210  
PRIOR FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US/09/934, 901  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229, 906  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 16  
LENGTH: 437  
TYPE: PR1  
ORGANISM: METHYLIOMONAS SP.  
US-10-321-210-16

Query Match 100.0%; Score 2284; DB 4; Length 437;  
Best Local Similarity 100.0%; Pred. No. 1,6e-215;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHYLTADIRFCHEWFLNFYTLNKKPKVAIITAGGLAPCLNSAIGSLIERYTE 60  
DB 1 DVVTWPHYLTADIRFCHEWFLNFYTLNKKPKVAIITAGGLAPCLNSAIGSLIERYTE 60  
QY 61 IDPSIEIICRGYKGLLDGSDYPTAEVRKKAQVLOFGSGVIGNSRVKLTNVKDCVR 120  
DB 61 IDPSIEIICRGYKGLLDGSDYPTAEVRKKAQVLOFGSGVIGNSRVKLTNVKDCVR 120  
QY 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLARNNYGLTVIGL.PKTV 180  
DB 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLARNNYGLTVIGL.PKTV 180  
QY 181 DNDVFPKISLGAWTAABEGARFEMNVVAENNANPRMLIVHEVMGRNCGLTAATQOYR 240  
DB 181 DNDVFPKISLGAWTAABEGARFEMNVVAENNANPRMLIVHEVMGRNCGLTAATQOYR 240  
QY 241 KLLDRAEWLPELGLTRSEYEVHAFVPEMAIDLEBAKRLREVMKVCVNI.FVSEGAGV 300  
DB 241 KLLDRAEWLPELGLTRSEYEVHAFVPEMAIDLEBAKRLREVMKVCVNI.FVSEGAGV 300  
QY 301 EAIIVAMQAKGQEVPRDAFGHILKDAVNPCKWFGQFQMGIGAEKTLVOKSGVFAPASAS 360  
DB 301 EAIIVAMQAKGQEVPRDAFGHILKDAVNPCKWFGQFQMGIGAEKTLVOKSGVFAPASAS 360  
QY 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESVIGHDEDENGVLAIEPRRIKGGKPFNIDTWENS 420  
QY 421 MLSEIGOPKGGKVEVSH 437  
DB 421 MLSEIGOPKGGKVEVSH 437

## RESULT 4

US-10-320-874-16  
Sequence 16, Application US/10320874  
Patent No. 6773905  
GENERAL INFORMATION:  
APPLICANT: Koffas, Matheos  
APPLICANT: Odom, J. Martin  
APPLICANT: No. 6773905ton, Kelley C.  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/10/320, 874  
PRIOR FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US/09/934, 901  
PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/229,306  
 ; PRIOR FILING DATE: September 1, 2000  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 16  
 ; LENGTH: 437  
 ; TYPE: PRT  
 ; ORGANISM: METHYLOMONAS SP.  
 ; US-10-320-874-16

Query Match 100.0%; Score 2284; DB 4; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-215;  
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTMPHLLTADIRFCMFLNFYTLNKKPKVAILLTGGLAPCLNSAIGSLIEYTE 60  
 DB 1 DVVTMPHLLTADIRFCMFLNFYTLNKKPKVAILLTGGLAPCLNSAIGSLIEYTE 60  
 QY 61 IDPSIEIICYRGYKGLLDSDYPTAEVRKKAQVLRFGGSVIGNSRVKLTNVKDCVKR 120  
 DB 61 IDPSIEIICYRGYKGLLDSDYPTAEVRKKAQVLRFGGSVIGNSRVKLTNVKDCVKR 120  
 QY 121 GLYKEGEDPQKVAADQVKKGVLDLHTTGDDTNTAAADLAFLARNNGLTIVGLPKTV 180  
 DB 121 GLYKEGEDPQKVAADQVKKGVLDLHTTGDDTNTAAADLAFLARNNGLTIVGLPKTV 180  
 QY 181 DNVVFPKOSLGAMTAEGARFPMNVVAENNAPRLIVHEWVGRNGMLTAATAQEYR 240  
 DB 181 DNVVFPKOSLGAMTAEGARFPMNVVAENNAPRLIVHEWVGRNGMLTAATAQEYR 240  
 QY 241 KLDRAEMLPELGLTRESYEVHAFVPEMAIDLEAKRLREWDKVCNIFVSEAGV 300  
 DB 241 KLDRAEMLPELGLTRESYEVHAFVPEMAIDLEAKRLREWDKVCNIFVSEAGV 300  
 QY 301 EAIVAEQAQGOEYPRAPFGHIKLDANVPKGFSEGOQMTGAECTIVKSGFAPASAS 360  
 DB 301 EAIVAEQAQGOEYPRAPFGHIKLDANVPKGFSEGOQMTGAECTIVKSGFAPASAS 360  
 QY 361 NVDDMLRKSQADLAVECAFRESGVIGHEDNGNVRATEPPIKSGKFPNIDTFENS 420  
 DB 361 NVDDMLRKSQADLAVECAFRESGVIGHEDNGNVRATEPPIKSGKFPNIDTFENS 420  
 QY 421 MLSEIGQPKGKVEVSH 437  
 DB 421 MLSEIGQPKGKVEVSH 437

RESULT 5  
 US-08-416-870C-4  
 ; Sequence 4, Application US/08416870C  
 ; Patent No. 5824862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HIYOSHI, TORU  
 ; APPLICANT: MINE, TOSHIKI  
 ; APPLICANT: KASAKA, KEISUKE  
 ; APPLICANT: TYSON, ROBERT HUM  
 ; APPLICANT: PAGE, ANTHONY MILES JOHN  
 ; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE  
 ; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR  
 ; TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
 ; STREET: PO BOX 747  
 ; CITY: FALL CHURCH  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22040-0747  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/416,870C  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MORPHY JR, GERALD M  
 ; REGISTRATION NUMBER: 28,977  
 ; REFERENCE/DOCKET NUMBER: 760-195P (PCT)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 205-8000  
 ; TELEFAX: (703) 205-8050  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 483 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-416-870C-4

Query Match 11.8%; Score 270; DB 2; Length 483;  
 Best Local Similarity 27.6%; Pred. No. 1e-17;  
 Matches 113; Conservative 53; Mismatches 175; Indels 68; Gaps 15;

QY 36 AILTAGGLAPCLNSAIGSLIERYTEIDPSIEIICYRGYKGLLDSDYPTAEVRKKAQV 95  
 DB 95 AILTAGGLAPCLNSAIGSLIERYTEIDPSIEIICYRGYKGLLDSDYPTAEVRKKAQV 95  
 QY 96 LQRFSGSVIGNSRVKLTNVKDCVKRGLVKEGEDPQKVAADQVKKGVLDLHTTGDDTNT 155  
 DB 152 IHRGGTITGTSR-----GHDKPKI-VDSIDRGINOVYIIGDGTOK 194  
 QY 156 AAADLAFLARNNGLTIVGLPKTVNDVFPKOSLGAMTAEGARFPMNVVAENNANP 215  
 DB 195 GAIVYQEVRRRLKAVVAGIPIKINDIDPVIDKSGFDPAVEAGRAIHAIVEASAE 254  
 QY 216 RMLIVHEWVGRNGMLTAATAQYRKLDRAEMLPELGLTRESYEVHAFVPEMAIDLEA 275  
 DB 255 NGIGVVMKMGYSGLTA-----MYATLASRDVLCIIPSPFYLEG 295  
 QY 276 EA-----KLEFWDKVCNIFVSEAGVAIVAEQAQGOEYPRAPFGHIKLDANV 328  
 DB 296 EGGILEYVERKRLDQDHMV---IIVAEGAGQLLAENLK--TSPAKDSGKGLHDV- 348  
 QY 329 PGKMFGEQ---PAOMIGAECTIVQ-KSGYFAPASASNVDDMLRKSQADLAVECAFRE 383  
 DB 349 -GLMISDKIAHAKIIPMPITLAKYIDPTMTAIVASMSNDN---YCTLLAOSCVHGVN 404  
 QY 384 SGVIGHDED--NGNVLRAIEFPPIKSGKFPNIDTD--WFNSMLSEIGQ 428  
 DB 405 AGYTGFTSLGVNCR-QTYIFPFRNITEKQNNVVITDRMMAR-LLSTNQ 451

RESULT 6  
 US-08-416-870C-6  
 ; Sequence 6, Application US/08416870C  
 ; Patent No. 5824862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HIYOSHI, TORU  
 ; APPLICANT: MINE, TOSHIKI  
 ; APPLICANT: KASAKA, KEISUKE  
 ; APPLICANT: TYSON, ROBERT HUM  
 ; APPLICANT: PAGE, ANTHONY MILES JOHN  
 ; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE  
 ; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR  
 ; TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
 ; STREET: PO BOX 747  
 ; CITY: FALL CHURCH  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22040-0747

```

;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/416,870C
;
; FILING DATE:
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: MURPHY JR, GERALD M
;
; REGISTRATION NUMBER: 28,977
;
; REFERENCE/DOCKET NUMBER: 760-195P (PCT)
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (703) 205-8000
;
; TELEFAX: (703) 205-8050
;
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 469 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-416-870C-6

```

```

Query Match      11.6%; Score 264.5; DB 2; Length 469;
Best Local Similarity 26.8%; Pred. No. 3,4e-17;
Matches 109; Conservative 56; Mismatches 173; Indels 69; Gaps 16;

```

```

QY 37 ILTAGGLAPCLNSAIGSLERYTEIDPSIEIICRYGKGLLLGDSYPTAVERKKAGVL 96
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 IYTCGLCGRLNTVIREIVCGLDNMGVSRVIGIGGIRKFPVACNTIDSP--KSVNQN 130
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 QREGGVIGNSRVKLTNNVXDCVKGEGEDPQKVAADQVLKVDVLIHTTGGDDTNTA 156
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 HKRGGTVLGTSR-----GGHDTMKI-VDSIQDRGINQYVIGGDTQRG 173
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 AADLAFLARNYGLVIGLPTVNDVPPIKOSLGATRAEGAAVPMVAENANR 216
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 174 AGVIFEEIRRGKLVAVAGIPKTIIDNDIPYIDRSFGPDVAEQAQAINAAHVEAGSAEN 233
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 MLIVHEMGRNCGMLTAATAQERYKLLDRAEMLPGLTRESYEVAVFPEMAIDLEAE 276
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 GIGLVLMGRHSFIA-----HYATLASR-----DVCCCLIPSPFLYEEB 274
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 A-----KRLREVMKVCVNI FVSEGAGVEAIVAEQAQGEVBRDAFGH-IKLDVAVN 328
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 GGLFRLYERLKRKNGHMV-----IVVAEGAGQKLIINTKESMG--KDSGNSITLDDV-- 324
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 329 PGKMFGEQPAQMTGAETLVQ---KSGFPAASASNVDDMLIKSCADLAVECAFRRES 384
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 325 -GLMISQKIKENFKKIKTTINLKYIDPTVMIRAIIPSNASDNVYCTLLAHRVHGAMAGYT 383
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 385 G-VIGHDENGNVLAIEPPI--KSGKPEINIDTFWNSMLSEIGQP 428
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 384 GFLVVG--QVNGRHC-YIPFRIITEKONKVSITDRMAR-LLSSTNP 426
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 7  
US-08-416-870C-2  
; Sequence 2, Application US/08416870C  
; Patent No. 5824862

```

; GENERAL INFORMATION:
;
; APPLICANT: HIYOSHI, TORU
;
; APPLICANT: MINE, TOSHIKI
;
; APPLICANT: KASAKURA, KEISUKE
;
; APPLICANT: TYSON, ROBERT HUM
;
; APPLICANT: PAGE, ANTHONY MILES JOHN
;
; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
;
; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR
;
; TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER
;
; NUMBER OF SEQUENCES: 23
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP

```

```

;
; STREET: PO BOX 747
;
; CITY: FALL CHURCH
;
; STATE: VA
;
; COUNTRY: USA
;
; ZIP: 22040-0747
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/416,870C
;
; FILING DATE:
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: MURPHY JR, GERALD M
;
; REGISTRATION NUMBER: 28,977
;
; REFERENCE/DOCKET NUMBER: 760-195P (PCT)
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (703) 205-8000
;
; TELEFAX: (703) 205-8050
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 485 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-416-870C-2

```

```

Query Match      11.5%; Score 262; DB 2; Length 485;
Best Local Similarity 25.7%; Pred. No. 6,2e-17;
Matches 113; Conservative 56; Mismatches 179; Indels 92; Gaps 17;

```

```

QY 7 YHLTADIRFCWHFFNFNFYTLNMRKKAVALITAGGLAPCLNSAIGSLERYTEIDPSIE 66
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 YFSSDDVNAAC-----IYTCGLCGRLNTVIREIVHSLDNYGVNK 125
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 IICRYGKGLLLGDSYPTAVERKKAGVLFQGGVIGNSRVKLTNNVXDCVKGVLVEG 126
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 VFGIDGGYRGFYSKNIINILTP---KTVNDIHKRGCTIIGSSR-----GG 166
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 EDPQKVAADQVLKVDVLIHTTGGDDTNTAADAFLARNYGLVIGLPTVNDVPP 186
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 HDTTKI-VDSIQDRGINQYVIGGDTQRGAAVIVIEEIRRRRLKVIAGIPTTINDIPV 225
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 IKOSLGATRAEGAAVPMVAENANRMLIVHEVMGRNCGMLTAATAQERYKLLDRA 246
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 IDKSGFQPTAVEAQRALNAAHVEAESAENGIGVYKLMGRYSGFIA----- 271
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 EWLPELGLTRESYEVAVFPEMAIDLEAE-----KRLREVMKVCVNI FVSEGAG 299
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 -----MYATLASRDVLCILIPSPFLYEGDGLFYEIEKRLKENGHMV-----IVIAEGAG 322
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 VEAIVAE--MQKAGQVPRDARGHITKLDVNPCKMFGGEQPAQMTGAETLVQ-----KSG 352
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 QELTAEENNAHANEQ--DASGNKLLQDV--GLMISQKIRDFH-ATKTKMPTITLYIDPT 376
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 353 YPARASASNVDDMLIKSCADLAVECAFRRESGVIGHED--NGNVLAIEPPIKSGKP 410
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 377 YMIRAVPSNASDN---VYCTLLAOSCHVGAAGAGYGTSGLVNGR-QYTIIPNRITEKQN 432
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 411 FNIDTD--WFNSMLSEIGQP 428
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 433 NVVITDRMAR-LLSSTNP 451
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 8  
US-09-902-540-16136  
; Sequence 16136, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.

```

1      RESULT 9
2      US-08-416-870C-10
3      Sequence 10, Application US/08416870C
4      Patent No. 5824862
5      GENERAL INFORMATION:
6      APPLICANT: HIYOSHI, TORU
7      APPLICANT: MINE, TOSHIKI
8      APPLICANT: KASNOKA, KEISUKE
9      APPLICANT: TYSON, ROBERT HUW
10     APPLICANT: PAGE, ANTHONY MILLES JOHN
11     TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
12     TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR
13     TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER
14     NUMBER OF SEQUENCES: 23
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
17     STREET: PO BOX 747
18     CITY: FALL CHURCH
19     STATE: VA
20     COUNTRY: USA
21     ZIP: 22040-0747
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

RESULT 10
US-09-489-039A-12258
: Sequence 12258 Application US/09489039A
: Patent No. 6610836
: GENERAL INFORMATION:
: APPLICANT: Gary Breton et. al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
: TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709.2004001
: CURRENT APPLICATION NUMBER: US/09/489,039A
: CURRENT FILING DATE: 2000-01-27
: PRIOR APPLICATION NUMBER: US 60/117,747
: PRIOR FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 14342
: SEQ ID NO 12258
: LENGTH: 338
: TYPE: PRF
: ORGANISM: Klebsiella pneumoniae
: US-09-489-039A-12258

```

Query Match 9.9%; Score 227; DB 4; Length 338;

Best Local Similarity 23.8%; Pred. No. 9.8e-14; Mismatches 102; Conservative 63; Mismatches 138; Indels 126; Gaps 19;

```

QY 13 IRECHWFLNFNYTLNKKKVAITLTAAGLAPCLNSAIGSLIERYTEIDPSIETICRG 72
DB 8 IIFC---FLSSEVVM-----KKIGVLTSGGDAPGMNAIRGVYR--AALTEGLEVGID 58
QY 73 GYKGL-----LLGDSIPVTAEVKKAAGVLOFGGSVIGNSRVKLTNVKDCVKGLVKEG 127
DB 59 GYLGLEDYRNVQIDRYSVSDMINR-----GGTEIGSAR--FPEFRE-----E 98
QY 128 DPOKVAADOLVKQGVILITITIGDDDTNTAAADLAFLARNNGVLTGIVGPKTYDNDVPFI 187
DB 99 HIRAVAIENMKKGLDALVYIGDGSYGMARL-----TENGFPCIGLPGITIDNDIKGT 152
QY 188 KOSLGAMTAEGGARYFMNVVAENNPRLIVHEWGRNCGMLTAATQOEYKLDRAE 247
DB 153 DYTIGFETLSTVEAIDRLDRTSSSHQRTSYV-EVMGRYCGDLTLAA-----IAGGE 206
QY 248 WL--PELGITRESYEVHAFVPEMAIDLEAEK-----RLREVMKVCVNIF 293
DB 207 FIMVPEVEYTRD-----DLVAEIKAGIAGKKAIVAITHEMCDVDELAZY 252
QY 294 VSRGAVE---AIVAEQAKGQEVPRDAFGHIKLDVNPQKMGEGQFQMIGAEKTLVQK 350
DB 253 IEKETRETRATVYLGHIQKGSVEPYDR-----LASRMGAYALIELL 295
QY 351 SGYFARASASNDVMDLIKSCADLAVECAFRESGVIGHDENGVLAIRAEPRKIGKRP 410
DB 296 QGHGGR-----CYGIQNEKLVHND-----IIDAIENMK-----RP 325
QY 411 FNIDTWFN 419
DB 326 FK--NDMLD 332

```

## RESULT 11

```

US-09-134-001C-3774
; Sequence 3774, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3774
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3774

```

Query Match 9.9%; Score 226.5; DB 3; Length 345;

Best Local Similarity 25.4%; Pred. No. 1.1e-13; Mismatches 105; Conservative 68; Mismatches 136; Indels 105; Gaps 19;

```

QY 26 YTLNKKKVAITLTAAGLAPCLNSAIGSLIERYTEIDPSIETICRGYKGLLDGSPV 85
DB 21 YVVM---KIAVLTSGDSPGMNAIVRAVTR--TALYNNIEVGVYGVYGLDDDDIHLK 75
QY 86 TAEVKKAGVLOFGGSVIGNSRVKLTNVKDCVKGLVKEGEPQVAAADQVKKGVDTL 145
DB 76 --ELGSGVDGTTOR--GGTFLFSAR-----CPQ---FKR--EDVRKKAILENKRKIEGL 120
QY 146 HTGGGDDTNTAAADLAFLARNNGVLTGIVGPKTYDNDVPFIKOSGAMTAAEGARYFM 205

```

DB 121 VVIGGDSYRGAQRISBECKE-----IQTIGIPGTTIDNDINGDPTIGFDTA-----L 168

QY 206 NVVAEN-----NANPRLIVHEWGRNCGMLTAATQOEYKLDRAEMLPELGLTBE 257

DB 169 NIIISVDKIRDTASSHATFTIV-EVMGRDCG-----DLALW--AGL--- 207

QY 256 SYEVHAFVPEMAIDLEAEKRLREVMKVCVNIFVSRGAVEVAIVAEQAKGQEVPR 317

DB 208 SVGAETIVLEVNITDKVAEKIEQIKGKHSL-----VVAEGCSGQECAD 258

QY 318 AFGHIKLDVNPQKMGEGQFQMIGAEKTLVQKSGYFARASASNDVMDLIKSCADLA 377

DB 259 LKRYINID-----TRVSLGHIGKGSPPSGADRYLASRLGGYAVE 298

QY 378 CAFRES---GVIGHDENGVLAIRAEPRKIGKRPITDWFNSMLSEIQ 427

DB 299 LKQGETAKVGSI-----RNNQLTSTPDEI-----FAESDRKFNSQWYELAK 341

## RESULT 12

```

US-09-543-681A-8337
; Sequence 8337, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8337
; LENGTH: 330
; TYPE: PRF
; ORGANISM: Proteus mirabilis
US-09-543-681A-8337

```

Query Match 9.6%; Score 220; DB 4; Length 330;

Best Local Similarity 28.9%; Pred. No. 4.6e-13; Mismatches 81; Conservative 40; Mismatches 95; Indels 64; Gaps 10;

```

QY 28 LNNKKKVAITLTAAGLAPCLNSAIGSLIERYTEIDPSIETICRGYKGLLDGSPVTA 87
DB 6 MVNGIKRIGVLTSGDAPGMNAIRGVYR--AALTEGLEVGIFPGYGLY----- 54
QY 88 EVRKKAGVLOF-----GGSVIGNSR---VKLTNVKDCVKGLVKEGDPQKVAADO 136
DB 55 ENRMKK--LDRFSVSDMINRGTFPLGSARFPEFREDNR-----AAIEN 97
QY 137 LVKQGVILITITIGDDDTNTAAADLAFLARNNGVLTGIVGPKTYDNDVPFIKOSGAMTA 196
DB 98 MKQNELDALVYIGDGSYLGAKL-----TEAGFPCIGLPGITIDNDVAGTDTYTGYPFA 151
QY 197 AEGARYFMNVVAENNPRLIVHEWGRNCGMLTAAT-----QEYKLDRA 246
DB 152 LETAVEAIDRLDRTSTSHRISIV-EVMGRYCGDLTLASAAGCEFFVVLPESELPEFRD 210
QY 247 EWLPELGITRESYEVHAFV-----VPEMAIDLEAEK 278
DB 211 ELLAEIKAGIERGKAIVAITHEVCDVHELARFIEAEIK 250

```

## RESULT 13

```

US-09-583-110-5099
; Sequence 5099, Application US/09583110
; Patent No. 6639703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATRHO-07A

```

33 KKAVALTAGLAPCLNSAIGSLIERYTEIDPSIEIICVRYGKGLLGDSYPTAAEVRKK 92  
2 KRAVAVITSGDADGMAAIAVVRQ--AISEGMEVFQIYDGYAGMVAEIHPLDA---AS 56  
93 AGVLQRFSGSVIGNSR---VKLTNVKDCVKGGLVEGEDPQKVAADQLVKGVDLIHTI 148  
57 VGDIIIRGGTFLHSARYPEPAQL-----EG---QKGIIEQLKKGIEGVVVI 100  
149 GGDGDTAAADLAFLARNNYGLTVIGLPTVNDVPIKOSIGAMWTAEGARYFNNAV 208  
101 GGGSGTHGAAURL-----TEHGPPALGPGTINDIVIDTFTIGFDPAVTT--MDADINKI 153  
209 AENNANPRMLIVHEVWGRNCG---WLTATAOEYRKLIDRAEWLDELGLTRE----- 257  
154 RDTSSSHRRFRFVEVWGRNAGDIALMAGINTGAD--EII-----IPAGFKMEDIVASIK 206  
258 -SYEV--HAFFVPEMAIDLEAF-AKRLREVMKVDVCNIFVSEGAVEAIVAEWQAKQ 312  
207 AGYECGKKNIIIVLAEGVMAAEFGQYKLEAGDTS---LRVTE-----LGHIGRGG 256  
313 EVPRDAFGHIKLDVAVNGKWFGEQFAMIGAEKTLVQXSG 352  
257 PTARD-----RVLASRMGAHVAVKLKEG 279

Query Match 9.6%; Score 220; DB 4; Length 335;  
Best Local Similarity 25.9%; Pred. No. 4.7e-13;  
Matches 88; Conservative 55; Mismatches 115; Indels 82; Gaps 16;  
CURRENT APPLICATION NUMBER: US/09/583.110  
CURRENT FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/107.433  
PRIOR FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/085.131  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: US 60/051.553  
PRIOR FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 5322  
SEQ ID NO 5099  
LENGTH: 335  
TYPE: PRN  
ORGANISM: Streptococcus pneumoniae  
US-09-583-110-5099

Query Match 9.6%; Score 218.5; DB 4; Length 321;  
Best Local Similarity 24.5%; Pred. No. 6.2e-13;  
Matches 92; Conservative 54; Mismatches 113; Indels 117; Gaps 15;  
33 KKAVALTAGLAPCLNSAIGSLIERYTEIDPSIEIICVRYGKGLLGDSYPTAAEVRKK 92  
3 KRIIGITSGDADGMAAIAVVRK--SIFDGIIEVGVINGYFAGLVAGD-----IR-- 51

93 AGVLQRFSGSVIGNSRVLKLTNVKDCVKG-----LVKGEEDPQKVAADQLVXD 140  
52 -----RLDVAADVGDKIQRGTFLYSARYPEFAEEG---QKGIIEQLKKE 93  
141 GVDIHTIGDDPTNTAAADLAFLARNNYGLTVIGLPTVNDVPIKOSIGAMWTAEG 200  
94 GIEGLVAVIGDGSYHGA-----MALTKRGFPVAVGIPGTINDI PGDTFTIGDTA---- 143  
201 ARFYNNVAEN-----NANPRMLIVHEVWGRNCGWLTATAOEYRKLIDRAEWLDEL 252  
144 -----INTVLESIDRIDTATSHRTFVI--EVMGRNAG-----DIALMSGVA 184  
253 GLTRSEYVAHAFVPEMAIDLEAARLRVMD--KVDVCNIFVSEGAVEAIVAEWQAK 310  
185 GGADE-----IIPHDPMKNVARIQEGDRGKHGCL--IILAEG----- 224  
311 GQEVPRDARGHITLDVAVNGKWFGEQFAMIGAEKTLVQXSGIFPAASASVNDMLIKS 370  
225 -----VMGNEPADKLSE--YGFHTRVSIIGHVVRGSGSPSARDVLAASK 267  
371 CADLAVECAFRRESGV 386  
268 FGSYAVELEKKGKGL 283

RESULT 15  
US-09-107-532A-6470  
Sequence 6470, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Denek  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6470:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...323





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2005, 10:07:54 ; Search time 5328 Seconds

(without alignments)  
496,422 Million cell updates/sec

Title: US-10-701-200-6

Perfect score: 2284

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-TRANS=humano.cdf -LIST=45 -DOCLIGN=200 -THR SCORE=0.5 -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEARSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10701200.QCGN\_1\_1\_733/runat\_31032005\_095523\_10864  
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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2284	100.0	1311	9	US-09-934-866-5
3	2284	100.0	1311	10	US-09-941-947A-1
4	2284	100.0	1311	15	US-10-320-924-15
5	2284	100.0	1311	15	US-10-320-874-15
6	2284	100.0	1311	15	US-10-363-567-1
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9	306.5	13.4	1050	17	US-10-369-493-31795
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19	270	11.8	1347	17	US-10-282-122A-11067
20	269.5	11.8	1023	15	US-10-156-761-2809
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22	267.5	11.7	3405	18	US-10-425-115-165105
23	263.5	11.5	2310	18	US-10-437-963-12274
24	262	11.5	960	17	US-10-369-493-26592
25	261	11.4	1035	17	US-10-369-493-42948
26	259	11.3	1958	18	US-10-437-963-6352
27	258.5	11.3	2363	18	US-10-425-115-121483
28	255	11.2	1677	17	US-10-425-114-8526
29	254	11.1	2149	17	US-10-424-599-128266
30	249.5	10.9	956	17	US-10-369-493-33339
31	249	10.9	2123	18	US-10-425-115-119704
32	248	10.8	1073	17	US-10-369-493-33356
33	246.5	10.8	2964	17	US-10-369-493-45685
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38	241.5	10.6	2412	17	US-10-424-599-115967
39	240.5	10.5	960	17	US-10-282-122A-36804
40	240.5	10.5	963	9	US-09-815-242-9687
41	240.5	10.5	963	17	US-10-282-122A-38849
42	240.5	10.5	963	17	US-10-282-122A-39841
43	239.5	10.5	3761	18	US-10-437-963-1690
44	238.5	10.4	963	9	US-09-815-242-6325
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ALIGNMENTS

RESULT 1

US-09-934-901-15

Sequence 15, Appl

Patent No. US2002011085A1

GENERAL INFORMATION:

APPLICANT: Koffas, Matheos

APPLICANT: Odom, J. Martin

APPLICANT: No. US2002011085A1ton, Kelley C.

APPLICANT: Ye, Rick

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CL1619 US NA

CURRENT APPLICATION NUMBER: US/09/934,901

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,906

PRIOR FILING DATE: September 1, 2000

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 15

LENGTH: 1311

TYPE: DNA

ORGANISM: METHYLOMONAS SP.  
US-09-934-901-15

## Alignment Scores:

Pred. No.:	4.08e-253	Length:	1311
Score:	2284.00	Matches:	437
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-701-200-6 (1-437) x US-09-934-901-15 (1-1311)

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QY 21 LeuAsnPheAsnPhetYrThrLeuMetAsnLysProLysValAlaIleLeuThrAla 40
DB 61 CTAACTTAACTTCTACACGCTCATGAACAACTTAAAGTTGCAATACCTGACAGCA 120
QY 41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGluArgTyrThrGlu 60
DB 121 GGGGCTTGCGCTGTTGTAATCCGCAATCGGATGGTATGATGCAAGCTTATACCGAA 180
QY 61 IleAsnProSerIleGluIleIleCysTyrArgGlyGlyTyrLysGlyLeuLeuLeuGly 80
DB 181 ATGATCCTTACGATTAAGTAATCATTTGCTATCGCGCGGTTATAAAGCCCTGTTGCGGC 240
QY 81 AsnSerTyrProValThrAlaGluValArgLysValAlaGlyValLeuGluArgPheGly 100
DB 241 GATTCCTTATCAGATTAACGGCCGCAAGCGGTAAGGCGGCTGTTGCAACGTTTGGC 300
QY 101 GlySerValIleGlyLysAsnArgValLysLeuThrAsnValLysAsnProCysValLysAsn 120
DB 301 GGTTCGTGATCGGCAACAGCCGCTCAAAATTGACCAATGTCAAGATCGCGTGAACGC 360
QY 121 GlyLeuValLysGlyGluGluAsnProGluLysValAlaAlaAsnGluLeuValLysAsn 140
DB 361 GGTTCGTGATCGGCAACAGCCGCTCAAAATTGACCAATGTCAAGATCGCGTGAACGC 420
QY 141 GlyValAlaPheIleLeuHisThrIleGlyLysAsnProThrAsnThrAlaAlaAsnLys 160
DB 421 GGTTCGTGATTCGTGACACCAATCGCGCGGATGATACCAATTCGCGACAGCGGATTTG 480
QY 161 AlaAlaPheLeuAlaArgAsnAsnTyrGlyLeuThrValIleGlyLeuProLysThrVal 180
DB 481 GCGCATTCCTGGCCAGAAATTAATTAAGGACTGACCGCTCATTTGCTTAAACCGTC 540
QY 181 AsnAsnAspValPheProIleLysGlnSerLeuGlyValATrThrAlaAlaGluGlnGly 200
DB 541 GATTAAGCATATTTCCGATCAAGCAATCATCTAGTCTTGGACCTCCCGCCAGCAAGGC 600
QY 201 AlaArgTyrPheMetAsnValValAlaGluAsnAsnAlaAsnProArgMetLeuIleVal 220
DB 601 GCCCGTTAATTCATGAACGTGGCGGCAAAACCAAGCCCAACGACGATGCTGATCGTA 660
QY 221 HisGluValMetGlyLysArgAsnGlyTyrTrpLeuThrAlaAlaAsnGluGlnGlyTyrArg 240
DB 661 CACGAAGTGAATGGCCGTAATCTGGCTGCTGACCGCTGCAACCGCGCAGGAATATCCG 720
QY 241 LysLeuLeuAspArgLysGluTrpLeuProGluLeuGlyLeuThrArgGluSerTyrGlu 260
DB 721 AAATTACTGACCGCTCCGAGTGGTTCGCGGAATTTGGGTTTGTGCTGTGAATTTTGA 780
QY 261 ValHisAlaValaPheValProGluMetAlaIleAsnLeuGluAlaGluAlaLysArgLeu 280
DB 781 GTGCAACGCGGTATTCCTTCGGAATAAGCGATGACCTGGAACCGCAAGCGCCCTG 840
QY 281 ArgGluValMetAsnLysValAspCysValAsnIlePheValSerGluGluValAlaGlyVal 300
DB 841 CGGAAAGTATGACAAAGTCGATTCGCTCAACATCTTGTTCGAAAGGTGCGGCGTC 900

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QY 301 GluAlaIleValaLysLeuMetGluAlaLysGlyGlnGluValaProArgAsnAlaPheGly 320
DB 901 GAACTATCTGTCGGGAAATGCAAGGCCAGGAAGTCCCGGCGATCGTTCCGCG 960
QY 321 HisIleLysLeuAspAlaValAsnProGlyLysTrpPheGlyGluGlnPheAlaGlnMet 340
DB 961 CACATCAACTGCAAGCGCTCAACCTGTGTAATGTTTCGGGACCAATTCGCGCAGAG 1020
QY 341 IleGlyAlaGluLysThrLeuValaGlnLysSerGlyTyrPheAlaArgAlaSerAlaSer 360
DB 1021 ATAGGCGCGAATAAACCTTGATACAAATAATCGGAATCTTCCCGCTCTTCTGCTTC 1080
QY 361 AsnValAspAsnMetArgLeuIleLysSerCysAlaAspLeuAlaValaGluCysAlaPhe 380
DB 1081 AACGTTGACGATCGATCGTTTGTATCAATCGTCGCGCATTCGCGCGTGAAGCGCGTTC 1140
QY 381 ArgArgGluSerGlyValIleGlyHisAsnGlyAsnAsnGlyValaValaIleLeuArgAlaIle 400
DB 1141 CCGCGCGAGTCTGGGCTGATCGCTACGACGACGACGACGACGACGACGACGACGACGAC 1200
QY 401 GluPheProArgIleLysGlyGlyLysProPheAsnIleAsnThrAsnTrpPheAsnSer 420
DB 1201 GATTTCCGCGCATCAAGGCGGCAACCGTTCAATATCGACACCGACTGTTCAATACG 1260
QY 421 MetLeuSerGluIleGlyGlnProLysGlyGlyLysValaGluValaSerHis 437
DB 1261 ATGTTGAGGAAATCGGCCACGCTTAAAGCCGTTAAAGTCGAAGTCAGGCAC 1311

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## RESULT 2

US-09-934-868-5  
Sequence 5, Application US/09934868  
Patent No. US20020137190A1

## GENERAL INFORMATION:

APPLICANT: Kofas, Matcheos  
APPLICANT: Odom, James M  
APPLICANT: Schenck, Andreas J  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1596 US NA  
CURRENT APPLICATION NUMBER: US/09/934,868  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,858  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 5  
LENGTH: 1311  
TYPE: DNA  
ORGANISM: METHYLOMONAS SP.  
US-09-934-868-5

## Alignment Scores:

Pred. No.:	4.08e-253	Length:	1311
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-701-200-6 (1-437) x US-09-934-868-5 (1-1311)

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DB 61 CTAACTTAACTTCTACACGCTCATGAACAACTTAAAGTTGCAATACCTGACAGCA 120
QY 41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGluArgTyrThrGlu 60
DB 121 GGGGCTTGCGCTGTTGTAATCCGCAATCGGATGGTATGATGCAAGCTTATACCGAA 180
QY 1261 IleAsnProSerIleGluIleIleCysTyrArgGlyGlyTyrLysGlyLeuLeuLeuGly 80

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 Db 241 GATTTCTATTCACATTAACGGCCGAAGTCCGTAAGAAAGCGGGTGTCTGCAACCTTTGGC 300  
 Qy 101 GlySerValIleGlyAenSerArgValIleLeuThrAsnValIleYsAspCysValIleYsArg 120  
 Db 301 GGTTCGTGTATCCGCAACAGCCCGCTAAATTGACCAATGTCAAAGACTCGTGAAACGC 360  
 Qy 121 GlyLeuValIleGlyGluGlyIleuAapProGlnIleValAlaIleAapGlnIleuValIleYsAsp 140  
 Db 361 GGTTCGTGTCAAGAGGGGTGAAGATCCGCAAAAAGTCCGGCTGATCAATTTGGTTAAGAT 420  
 Qy 141 GlyValIleAspIleLeuHsrThrIleGlyIleYsAspThrAsnThrAlaAlaIleAapLeu 160  
 Db 421 GGTGTGATATTCGACACCATCGCGCGGATGATCCAAATACGCGCAGCAGCGGATTTG 480  
 Qy 161 AlaAlaPheLeuAlaArgAenArgValIleuThrValIleGlyLeuProLysThrVal 180  
 Db 481 GCAGCATTTCTGGCCGAATAATTAACGACTGCGCTCATTTGATTAACCTAAACCGTC 540  
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 Db 541 GATACGAGCATTTCCGATCAAGCATCACTAGTCTTGATGCTGCGCGCGCAAGC 600  
 Qy 201 AlaArgTyrPheMetAsnValIleAlaGluAsnAsnAlaAsnProArgMetLeuIleVal 220  
 Db 601 GCCGCTTATTCATGAACGTGGTGGCCGAATAACCCCAACCCCAACCATGCTGATCTGTA 660  
 Qy 221 HisGluValMetGlyArgAenCysGlyTrpLeuThrAlaAlaThrIleGlnGluTyrArg 240  
 Db 661 CACGAAGTGAATGGCCGTAACCTGGCTGCTGACCTGCACACCGCGCGGAATATCGC 720  
 Qy 241 LysLeuLeuAspArgAlaGluTrpLeuProGlnLeuGlyLeuThrArgGluSerTyrGlu 260  
 Db 721 AATTTACTGACCGCTGCGAGTGGTCCGGAATGGCTTGACTCTGATCTTATGA 780  
 Qy 261 ValHisAlaValPheValProGlnMetAlaIleAapLeuGlnAlaGluAlaLysArgLeu 280  
 Db 781 GTCCACCGCGTATTCGTTCCGGAATAGCGCATCGACCTGGAAGCCGAAGCCGAGCTG 840  
 Qy 281 ArgGluValMetSerLysValAspCysValAsnIlePheValSerGluGlyAlaGlyVal 300  
 Db 841 CGGGAAGTGAACAAAGTCGATGCGCAACATCTTCCGTAAGGTGCGCGGCTC 900  
 Qy 301 GluAlaIleValAlaGlnMetGlnAlaLysGlyGlnGluValProArgAspAlaPheGly 320  
 Db 901 GAAGCTATCTCGCGGAATCGCAGGCCCAAGGCCCAAGAGTCCGCGCATGCGCTTCCG 960  
 Qy 321 HisIleLeuLeuAspAlaValAsnProGlyLysTrpPheGlyGluGlnPheAlaGlnMet 340  
 Db 961 CACATCAAACTGATGGGTCAACCTCGTAATGTTGCGCGAGCAATTCGCGAGATG 1020  
 Qy 341 IleGlyAlaGluLysThrLeuValGlnLysSerGlyTyrPheAlaArgAlaSerAlaSer 360  
 Db 1021 ATAGGCGCGGAAAAAACCTCGTAACAAATCCGGGATACCTTCCGCTGCTTCTGCTCC 1080  
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 Qy 401 GluPheProArgIleLysGlyLysPheProPheAsnIleAspThrAspTrpPheAsnSer 420  
 Db 1201 GAAGTTCCGCGCATCAAGGGCGGGAACCGTTCAATTCACACCGCATGCTGTAATGAC 1260  
 Qy 421 MetLeuSerGluIleGlyGlnProLysGlyLysValGluValSerHis 437

Db 1261 ATGTTGAGCAAAATCGCGCAGCTTAAGCGGTAAGTCGAAGTCAGCCAC 1311  
 RESULT 3  
 US-09-941-947A-1  
 ; Sequence 1, Application US/0941947A  
 ; Publication No. US20030003528A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brzostowicz, Patricia C.  
 ; APPLICANT: Cheng, Qiong  
 ; APPLICANT: Dicosimo, Deana J.  
 ; APPLICANT: Kofias, Mathews  
 ; APPLICANT: Miller, Edward S. Jr.  
 ; APPLICANT: Odom, J. Martin  
 ; APPLICANT: Picataggio, Steve  
 ; APPLICANT: Ruviviere, Pierre E.  
 ; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE  
 ; FILE REFERENCE: CL1903 US NA  
 ; CURRENT APPLICATION NUMBER: US/09/941,947A  
 ; PRIOR FILING DATE: 2001-09-01  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 1  
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 ; TYPE: DNA  
 ; ORGANISM: Methylobionas 16a  
 US-09-941-947A-1

Alignment Scores:  
 Pred. No.: 4.08e-253 Length: 1311  
 Score: 2284.00 Matches: 437  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-10-701-200-6 (1-437) x US-09-941-947A-1 (1-1311)

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 Db 1 GATGTGTCACATGCGCCCTATCTTAACGCGCTGAATTCGATTTGTCTATGCTTTT 60  
 Qy 21 LeuAsnPheAsnPheTyrThrLeuMetAsnLysProLysValAlaIleLeuThrAla 40  
 Db 61 CTTAACCTTAACCTTCAACGCTCATGAACAAACCTAAAGTTCCTAATACGACAGCA 120  
 Qy 41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGluArgTyrThrGlu 60  
 Db 121 GGGGGCTTGGCGCTTGTGTAATTCGCAATCGTAAGTTGATCGCAAGTTATACCGAA 180  
 Qy 61 IleAspProSerIleGluIleIleCysTyrArgGlyIleTyrLysGlyLeuLeuLeuGly 80  
 Db 181 ATGATCTTACGATTAACATTAATCATTTCTATCCGGCGGCTTATTAAGCCTGTGGCG 240  
 Qy 81 ApsSerTyrProValThrAlaGluValArgLysValAlaIleValLeuGlnArgPheGly 100  
 Db 241 GATTTCTTACCACTTAACGCGCGAAGTGCCTAAAGCGGGGTCTTGCACGTTTGGCG 300  
 Qy 101 GlySerValIleGlyAenSerArgValIleLeuThrAsnValIleYsAspCysValIleYsArg 120  
 Db 301 GGTTCGTGTATCGCAACAGCCCGTCAAAATTAAGCAATGTCAAAAGACTGCGTAACCG 360  
 Qy 121 GlyLeuValIleGlyGluGlyIleuAapProGlnLysValAlaIleAapGlnIleuValIleYsAsp 140  
 Db 361 GGTTCGTGTCAAGAGGGGTGAAGATCCGCAAAAAGTCCGGCTGATCAATTTGGTTAAGAT 420  
 Qy 141 GlyValIleAspIleLeuHsrThrIleGlyIleYsAspThrAsnThrAlaAlaIleAapLeu 160  
 Db 421 GGTGTGATATTCGACACCATCGCGCGGATGATGATACCAATACGCGCAGCAGGATTTG 480

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QY 161 AAlaIaPheLeuValaArgAnaenTyrgLYLeuThraIIeGLyLeuProLYstrThraI 180
| | | | |
DB 481 GCAGCATTCCTGGCCGAAATAATATACGACCTGATCGTATGTTACTTAACCAACCGTC 540
| | | | |
QY 181 AAPAAnaPValaPheProIIeLYrgInserLeuGLYAlaTrpThraIaAlaGLInGLngLY 200
| | | | |
DB 541 GATTAACGACGATATTCGATCAAGCAATCACTAGGTCCTTGACCTCCCGCGAAGAGC 600
| | | | |
QY 201 AAlaArgTYrPheMeCAsnValaIaGLuaAsnAnaIaAsnProArgMeCLeuIleVal 220
| | | | |
DB 601 GCGCGTATTATTCATGAACGTCGTCGCGAANAACAGCCCAACCATGCTGATCGTA 660
| | | | |
QY 221 HLeGLYValaMeCGLYArGaenCYrgLYTrpLeuThraIaAlaThraIaGLInGLYArg 240
| | | | |
DB 661 CACGAAGTGTGGCCGTAACTCGCGCTGCTACCGCTGCACCGCGCAAGAAATATCCG 720
| | | | |
QY 241 LysLeuLeuAspArgAlaGLUTrPLeuProGLInLeuGLYLeuThraArgGLInserTYrgLU 260
| | | | |
DB 721 AATTTACTGACCGTCGCGAGTGTGCGGAAATGGGTTTGACTCGTGAATCTTAATGA 780
| | | | |
QY 261 ValHIsAlaValaPheValProGLInMeCAlaIleAspLeuGLuaGLuaIaLysArgLeu 280
| | | | |
DB 781 GTTCACGCGGTATTCGTTCCGAAATGCGCATGACCTGGAACCGAAGCCAGCCGCTG 840
| | | | |
QY 281 ArgGLYValaMeCAsnLYsValaAspCYsValaAsnIlePheValserGLYAlaGLYVal 300
| | | | |
DB 841 CCGGAAGTGTATGACAAAGTCGATGCGTCAATCTTGCTTCCGAAGGTGCGCGCTG 900
| | | | |
QY 301 GLuaIaIleValaIaGLInMeCGLuaIaLYsGLYGLInGLYValProArgAspAlaPheGLY 320
| | | | |
DB 901 GAAGCATATCGTCGCGAANAAGCAGGCGCAAGCCAGAAAGTCGCGCATGCGTTCGCG 960
| | | | |
QY 321 HIsIleLYsLeuAspAlaValaAsnProGLYLYsTrpPheGLYGLInPheIaGLInMeC 340
| | | | |
DB 961 CACATCAAACTGATGCGGTCACCTCGTGAATGCTTCGCGACCAATTCGCGCAAGT 1020
| | | | |
QY 341 ILeGLYAlaGLYLYsThraLeuValaGLInLYsSerGLYTYrPheAlaArgAlaSerAlaSer 360
| | | | |
DB 1021 ATAGCGCGCGAANAACCTCGTACAAATCGGAAATCGGAAATCTGCGCTGTTGCTTC 1080
| | | | |
QY 361 AsnValaAspAspMeCArgLeuIleLYsSerCYsAlaAspLeuAlaValGLYsAlaPhe 380
| | | | |
DB 1081 AAGGTGACGACATGCGTTGATCAATCTGCGCGACCTTGCGCGTGCAGTCCGCTTC 1140
| | | | |
QY 381 ArgArgGLYserGLYValaIleGLYHIsAspGLYAspAsnGLYAsnValaLeuArgAlaIle 400
| | | | |
DB 1141 CCGCGGAGTCTGCGCTGATCGGTCACAGCAAGACACACGCAACGTGTGCTGCGATC 1200
| | | | |
QY 401 GLUPheProArgIleLYsGLYGLYsProPheAsnIleAspThraAspTrpPheAsnSer 420
| | | | |
DB 1201 GAGTTTCCGCGCATCAAGCGCGCAACCGTTCAATATGACACGCACTGTTCAATAGC 1260
| | | | |
QY 421 MetLeuSerGLYIleGLYGLInProLYsGLYLYsValaGLYValserHIs 437
| | | | |
DB 1261 ATGTTAGCGAAATCGCGCACCTAAAGCGGTAAAGTCGAAGTCAAGTCAAGCCAC 1311
| | | | |
RESULT 4
US-10-320-924-15
; Sequence 15: Application US/10320924
; Publication No. US20030129721A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Mathios
; APPLICANT: Odem, J. Martin
; APPLICANT: No. US20030129721A1ton, Kelley C.
; APPLICANT: Ye, Rick
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: CUI619 US NA
; CURRENT APPLICATION NUMBER: US/10/320,924
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/934,901
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,906
; PRIOR FILING DATE: September 1, 2000

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: METHYLOMONAS SP.
US-10-320-924-15

Alignment Scores:
Pred. No.: 4,086-253 Length: 1311
Score: 2284.00 Matches: 437
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-701-200-6 (1-437) x US-10-320-924-15 (1-1311)
QY 1 AAPValaIThrTrpProTYrHIsLeuThraIaAspIleArgPheCYsHIsTrpPhePhe 20
| | | | |
DB 1 GATGTGTCACATGAGCCCTATCATCTTAACGCGTGATATTCGATTTGTGATGTTTTT 60
| | | | |
QY 21 LeuAsnPheAsnPheTYrThraLeuMeCAsnLYsProLYsValaIaIleLeuThraIa 40
| | | | |
DB 61 CTTAACTTTAACTTCTTACACGCTCATGAACAAACCTTAACCAAGTTGCATCTGACAGCA 120
| | | | |
QY 41 GLYGLYLeuAlaProCYsLeuAsnSerAlaIleGLYserLeuIleGLYArgTYrThraGLU 60
| | | | |
DB 121 GCGCGCTTGCGCCCTGTTGTTTAATTCGCAATCGGTAGTTTGAATGACGTTATACCA 180
| | | | |
QY 61 ILeAspProSerIleGLYIleCYsTYrArgGLYTYrLYsGLYLeuLeuLeuGLY 80
| | | | |
DB 181 ATCGATCCAGCATGAATCATTTGCTATGCGCGGTATTAAGCGCTGTGCTGGCG 240
| | | | |
QY 81 AspSerTYrProValaIThrAlaGLYValaArgLYsAlaGLYValleuGLInArgPheGLY 100
| | | | |
DB 241 GATTTCTTATCCAGTAAACCGCCGCAAGTGGGTAAAGGCGGGGTCTCGCAAGTTTTTGGC 300
| | | | |
QY 101 GLYserValIleGLYAsnSerArgValLYsLeuThraAsnValLYsAspCYsValLYsArg 120
| | | | |
DB 301 GGTTCGTGATCGGCAACGCGCGTCATTAATGACCAATGTAAGACTGCGTGAACCC 360
| | | | |
QY 121 GLYLeuValLYsGLYGLYsAspProGLInLYsValaIaAlaAspGLInLeuValLYsAsp 140
| | | | |
DB 361 GGTTTGTCAAAGAGGTGAAGATCCGCAAAAAGTCGGCGTCGATCAATGTTAGAT 420
| | | | |
QY 141 GLYValaAspIleLeuHIsThraIleGLYGLYsAspThraAsnThraIaAlaAspLeu 160
| | | | |
DB 421 GGTGTGATATTTCTCACACCATCGCGCGCATGATCCCAATACGCGACGCGGATTTG 480
| | | | |
QY 161 AlaIaPheLeuAlaArgAsnAsnTYrGLYLeuThraIleGLYLeuProLYsThraI 180
| | | | |
DB 481 GGAGCATTCCTGCCGAAATAATTAACGACTGACCGCTATGTTACTTAACCAACCGTC 540
| | | | |
QY 181 AAPAAnaPValaPheProIIeLYsGLInserLeuGLYAlaTrpThraIaAlaGLInGLngLY 200
| | | | |
DB 541 GATTAACGACGATATTCGATCAAGCAATCACTAGGTCCTTGACCTCCCGAAGAGC 600
| | | | |
QY 201 AAlaArgTYrPheMeCAsnValaIaGLuaAsnAnaIaAsnProArgMeCLeuIleVal 220
| | | | |
DB 601 GCGCGTATTATTCATGAACGTCGTCGCGAANAACAGCCCAACCATGCTGATCGTA 660
| | | | |
QY 221 HLeGLYValaMeCGLYArGaenCYrgLYTrpLeuThraIaAlaThraIaGLInGLYArg 240
| | | | |
DB 661 CACGAAGTGTGGCGGTAACTCGCGCTGCTACCGCTGCACCGCGCAAGAAATATCCG 720
| | | | |
QY 241 LysLeuLeuAspArgAlaGLUTrPLeuProGLInLeuGLYLeuThraArgGLInserTYrgLU 260
| | | | |
DB 721 AATTTACTGACCGTCGCGAGTGTGCGGAAATGGGTTTGACTCGTGAATCTTAATGA 780
| | | | |
QY 261 ValHIsAlaValaPheValProGLInMeCAlaIleAspLeuGLuaGLuaIaLysArgLeu 280
| | | | |
DB 781 GTTCACGCGGTATTCGTTCCGAAATGCGCATGACCTGGAAGCCGAAGCCAGCGCGCTG 840
| | | | |

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QY 281 ArgGluValMetAspLysValAspCysValAsn1IephValSerGluGlyValI 300  
 DB 841 CGCGAAGTGAATGACAAAGTCGATTCGATCAACATCTTCTCCGAAAGTCCGGCGTC 900  
 QY 301 GluAlaIleValAlaGluMetGlnAlaLysGlyGlnGluValProArgAspAlaPheGly 320  
 DB 901 GAAGCTATCGTCCGCGAAATGACAGGCCAAGGCCAGAAAGTCCGGCGCATGGCTTCGGC 960  
 QY 321 HisIleLysLeuAspAlaValAsnProGlyLysTrpPheGlyGluGlnPheAlaGlnMet 340  
 DB 961 CACATCAAACTGATCGGTCACACCTCGTAAATGTTCCGCGACAGCAATTCGGCGAGATG 1020  
 QY 341 IleGlyAlaGluLysTrpLeuValGlnLysSerGlyTrpPheAlaArgAlaSerAlaSer 360  
 DB 1021 ATAGCGCGCGAAAAAACCTCGGTACAAAATCCGGATCTTCCGCCGCTTCTGCTTCC 1080  
 QY 361 AsnValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPhe 380  
 DB 1081 AACGTTGACGACATGGCTTGCATCAATCGTGGCGCGACTTGGCGGTGCGATCGCGCTTC 1140  
 QY 381 ArgArgGluSerGlyValIleGlyHisAspGluAspAsnGlyAsnValLeuAlaGlyAlaIle 400  
 DB 1141 CGCGCGAGTCTGCGGTGATCGGTCAACGAAAGACAAACGCGCAACGTGTGCGTGGCATC 1200  
 QY 401 GluPheProArgIleLysGlyLysProPheAsnIleAspThrAspTrpPheAsnSer 420  
 DB 1201 GACTTTCGCGCATCAAGGGCGCAACCGTTCAATTCGACACCGCATGCTGTTCAATGAC 1260  
 QY 421 MetLeuSerGluIleGlyGlnProLysGlyGlyLysValGluValSerHis 437  
 DB 1261 ATGTTAGCGAATTCGGCCAGCCTTAAAGCGGTAAAGTGAAGTCAAGCCAC 1311

## RESULT 5

US-10-320-874-15  
 ; Sequence 15, Application US/10320874  
 ; Publication No. US20030138909A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koffee, Matheos  
 ; APPLICANT: Odom, J. Martin  
 ; APPLICANT: No. US20030138909A1ton, Kelley C.  
 ; CAPT: Ye, Rick  
 ; TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN  
 ; FILE REFERENCE: CL1619 US NA  
 ; CURRENT APPLICATION NUMBER: US/10/320,874  
 ; CURRENT FILING DATE: 2002-12-17  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/229,906  
 ; PRIOR FILING DATE: September 1, 2000  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 15  
 ; LENGTH: 1311  
 ; TYPE: DNA  
 ; ORGANISM: METHYLOMONAS SP.  
 US-10-320-874-15

## Alignment Scores:

Pred. No.: 4,08e-253 Length: 1311  
 Score: 2284.00 Matches: 437  
 Percent Similarity: 100.00% Conservative: 0  
 Basic Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

US-10-701-200-6 (1-437) X US-10-320-874-15 (1-1311)

QY 1 ArgValAlaThrTrpProGlyTrpHisLeuThrAlaAspIleArgPheCysHisTrpPhePhe 20  
 DB 1 GAGTGTGTCACAGCGCCCTATCACTTAAACGCTGATATCGATTGTCATTTGCTTTT 60  
 QY 21 LeuAsnPheAsnPhenThyTrpLeuMetAsnLysProLysValAlaIleLeuThrAla 40

DB 61 CTTAACTTAACTTACACGCTCATGACAAACCTAAAAAGTTGCATATCGACAGCA 120  
 QY 41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGluArgTrpThrGlu 60  
 DB 121 GGGCGCTTGCGCTTGTGTTGAATTCGCAATCGGTATGTTATCGAAAGTTATACCGAA 180  
 QY 61 IleAspProSerIleGluIleIleCysTrpArgGlyGlyTrpLysGlyLeuLeuGly 80  
 DB 181 ATCATCTTACGATTAATAATCATTTGCTATCCGCGCGCTTATTAAGGCTTGTCTGGCG 240  
 QY 81 AspSerTrpProValThrAlaGluValArgLysValGlyValLeuGlnArgPheGly 100  
 DB 241 GATCTTATCCAGTAAACGCGCCGAAGCGGTAAGGCGGAGTTCGCAACGTTTGGC 300  
 QY 101 GlySerValIleGlyAsnSerArgValLysLeuThrAsnValLysAspCysValLysArg 120  
 DB 301 GGTTCGTGATCGGCAACAGCCCGCTCAAAATTGACCAATGTCMAAGACTGCGGAACGC 360  
 QY 121 GlyLeuValLysGluGlyGluAspProGlyLysValAlaAlaAspGlnLeuValLysAsp 140  
 DB 361 GGTTCGTCAAGAGGGGTGAAGATCCGCAAAAGTCGCGCTGATCAATTGTTAAGAT 420  
 QY 141 GlyValAspIleLeuHisThrIleGlyLysAspAspThrAsnThrAlaAlaAspLeu 160  
 DB 421 GGTGTCGATATTCGACACACATCGCGCGCATGATACCAATACGCGACGACGATTTG 480  
 QY 161 AlaAlaPheLeuAlaArgAsnAsnTrpGlyLeuThrValIleGlyLeuProLysThrVal 180  
 DB 481 GCAGCATTCCTCGCCCAAAATATTAATGACGATGACCGTCATGCTTAAACCCGTC 540  
 QY 181 AspAsnAspValPheProIleLysGlnSerLeuGlyValaThrThrAlaGluGlnGly 200  
 DB 541 GATACGACGATATTCGATCAAGCAATCACTAGGCTTGACGTCGCGCGCAAGGC 600  
 QY 201 AlaArgTrpPheMetAsnValValAlaGluAsnAsnAlaAsnProArgMetLeuIleVal 220  
 DB 601 GCGCGTATTTATGACGACGATGCGGCGGAAACAAACGCCAACCGCATGCTGATCGTA 660  
 QY 221 HisGluValMetGlyArgAsnGlyTrpLeuThrAlaAlaThrAlaGlnGlyArg 240  
 DB 661 CACGAAGTATGGCGCGTAACTCGCGCTGCTGCAACCGCGCAACCGCGAAGTAATCCG 720  
 QY 241 LysLeuLeuAspArgIleGluTrpLeuProGlyLysGlyLeuThrArgGluSerTrpGlu 260  
 DB 721 AATTAATGACCGCGCGACGATGTTGCGGAATGGGTTTGAATCTGTAATCTTATGAA 780  
 QY 261 ValHisAlaValPheValProGluMetCAlaIleAspLeuGluValaGluAlaLysArgLeu 280  
 DB 781 GTGCACGCGGTATTCGTTCCGAAATGGCGATCGACTGGAACCGCAAGCCGCGCTG 840  
 QY 281 ArgGluValMetAspLysValAspCysValAsnIlePheValSerGluGlyAlaGlyVal 300  
 DB 841 CGCGAAGTATGACCAAGTCGATTCGTCACATCTTGTGTTCCGAAGTGGCGCGCTC 900  
 QY 301 GluAlaIleValAlaGluMetGlnAlaLysGlyGlnGluValProArgAspAlaPheGly 320  
 DB 901 GAAGCTATCGTCCGCGAAATGCAAGCCAAAGCCAGAAAGTCCGCGCATGTGCTCGCG 960  
 QY 321 HisIleLysLeuAspAlaValAsnProGlyLysTrpPheGlyGluGlnPheAlaGlnMet 340  
 DB 961 CACATCAAACTGATCGGTCACACCTGTAATGTTGCGCGACGCAATTCGCGCGAGATG 1020  
 QY 341 IleGlyAlaGluLysTrpLeuValGlnLysSerGlyTrpPheAlaArgAlaSerAlaSer 360  
 DB 1021 ATAGCGCGCGAAAAAACCTCGGTACAAAATCGGATCACTTCCGCCGCTTCTGCTTCC 1080  
 QY 361 AsnValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPhe 380  
 DB 1081 AACGTTGACGACATGGCTTGCATCAATCGTGGCGCATGCTGCGGTGCAAGTCCGGCTTC 1140  
 QY 381 ArgArgGluSerGlyValIleGlyHisAspGluAspAsnGlyAsnValLeuArgAlaIle 400

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Db      1141 CCGCCGAGTCTGCGGTGATCGGTCAAGCAAGAACGCAACGCTGTGCGTGCATC 1200
Qy      401 GIUPHPRGARGIIEIYAGIYLYSPROPHEAENIIEASPHRTPPHEANSER 420
Db      1201 GAGTTTCCCGCATCAAGGCGGCAACCGTTCAATGACACCGACTGGTTCAATGAC 1260
Qy      421 MetLeuSerGIuIleGIYnProLYSGLIYLYVAIGIuValSerHis 437
Db      1261 ATGTTGAGGAATCGGCCAGCTTAAGCGGTAAAGTGAAGTCAAGCCAC 1311

RESULT 6
US-10-363-567-1
; Sequence 1, Application US/10363567
; Publication No. US2004007068A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours & Company
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: C11903 PCT
; CURRENT APPLICATION NUMBER: US/10/363,567
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/229858
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/229907
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Methylobionas 16a
US-10-363-567-1

Alignment Scores:
Pred. No.:      4,086-253      Length:      1311
Score:          2284.00      Matches:      437
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             17          Gaps:          0

US-10-701-200-6 (1-437) x US-10-363-567-1 (1-1311)
Qy      1 AepValIaIhThrTrpProTYRHisLeuThrAlaAspIIEArpPheCYsHisTrpPhe 20
Db      1 GATGTGTCACATGCGCCCTTATCTTACACGCGCTGAATTCGATTTGCTATGCTTTT 60
Qy      21 LeuAsnPhaAsnHeTYRThrLeuMetAsnLYSProLYSGLIYLYVAIAIIEuThra 40
Db      61 CTAACTTAACTTCTTACACGCTCATGACAACTTAAAGTTGCAATGACATGACAGCA 120
Qy      41 GIYGLYLeuAlaProCYLeuAsnSerAlaIIEGLYSerLeuIIEGLuArgTYRThrGIu 60
Db      121 GGGGGCTTGGCGCTTGTGTAATCCGCATCGGTAGTTGATCGAAGTTATACCGAA 180
Qy      61 ILeAspProSerIIEGLIuIIEIIECYsTYRArgGLIYLYTYRISGLYLeuLeuGLY 80
Db      181 ATCGATCTTACGATTAAGATCATTTGCTATCGCGCGTTATTAAGGCTGTGCTGGCG 240
Qy      81 AspSerTYRProValThrAlaGIuValArgLYSGLIYLYValleuGLnArgPheGLY 100
Db      241 GATTTCTTATCCAGTAAACGCGCGAAGTGGCGTAAAGGCGGGTGTCTGCAACGTTTGGC 300
Qy      101 GYSerValIIEGLIYAsnSerArgValLYSLeuThrAsnValLYSAspCYsValLYSArg 120
Db      301 GGTTCGTGTATCGGCAACAGCCCGCTCAATTTACCAATGTCAAAAGACTGCGGTAAACGC 360
Qy      121 GLYLeuValLYSGLIYGLIuAspProGLnLYSValAlaAlaAspGLnLeuValLYSAsp 140
Db      361 GGTTCGTCAAAAGGCTGAAGATCCGCAAAAGTGGCGGCTATCAATTTGTTAGGAT 420
Qy      141 GLYValAspIIEuHisTrhIIEGLIYAspAspThrAsnThraAlaAlaAspLeu 160
Db      421 GGTGTGATATTGTGACACCAATCGCGGGGATGATACCAATTCGCGAGAGAGGATTTG 480

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Qy      161 AlaAlaPheLeuAlaArgAsnAsnTYRGLYLeuThrValIIEGLYLeuProLYSThrVal 180
Db      481 GCGCATTTCTCGGCCAGAAATTAATTCAGACTGACCGCTCATTTGTTACTTAAACCGTC 540
Qy      181 AspaAspValIIEProIIELYSGLnSerLeuGLYAlaTrpThrAlaAlaGLnGLnGLY 200
Db      541 GATTAACGATTTTCCGATCAAGCATCATCTAGGTGCTTGACCTGCGCCGAGCAAGGC 600
Qy      201 AlaArgTYRPhMetAsnValValAlaGLIuAsnAsnAlaAsnProArgMetLeuIIEVal 220
Db      601 GCGCGTTATTTTCATTAAGAGTGTGCGCCAAACACCGCCACCATGCTGATTCGTA 660
Qy      221 HisGLIuValIIErGLIYArgAsnCYsGLIYTrpLeuThrAlaAlaThrAlaGLnGLYArg 240
Db      661 CACGAAGTATGAGCGCTGATCGCGGCTGCTGACCGCTGCACCGCGCAGAAATTCGC 720
Qy      241 IYSLeuLeuAspArgAlaGLIuTrpLeuProGLIuLeuGLYLeuThrArgGLnSerTYRGIu 260
Db      721 AATTACTGACCGTGGCGAGTGGTGGCGGAATGGGTTGACTCGTGAATCTTATGAA 780
Qy      261 VALHISAlaValIIEPheValProGLIuMetAlaIIEAspLeuGLIuAlaLYSArgLeu 280
Db      781 GTGACGCGGTATTTGTTCCGGAATGGCGATCGACTGGAAAGCCGAAGCGCGCTG 840
Qy      281 ArgGLIuValIIErAspLYSValAspCYsValAsnIIEPheValSerGLIuGLYAlaGLYVal 300
Db      841 CCGGAAGTATGACAAAGTGCATTCGTCACATCTTCTGTTCCGAAGTCCGGCGTC 900
Qy      301 GIuAlaIIEValAlaGLIuMetGLnAlaLYSGLIuGLnGLIuValProArgAspAlaPheGLY 320
Db      901 GAAGCTATCGTGGCGGAATGACAGGCCAAAGGCCAGAAATGCCGCGCATCGTTCCGC 960
Qy      321 HisIIELYLeuAspAlaValAsnProGLIYTrpPheGLIYGLnIIEPheAlaGLnMet 340
Db      961 CACATCAACCTGGAAGCGGTCAACCTGTGAATGTGTTCGGGACCAATTCGCGAGAGT 1020
Qy      341 IIEGLYAlaGLIuLYSLeuValGLIuLYSserGLIYTYRPhaAlaArgAlaSerAlaSer 360
Db      1021 ATAGCGCGGAAATCCCTGTGTACAAATGGGATTTCTGCGCGCTTCTGCTTCC 1080
Qy      361 AsnValAspAspMetArgLeuIIELYSserCYsAlaAspLeuAlaValGLIuCYsAlaPhe 380
Db      1081 AACGTTGACGATCGCTTATCAATCGTGGCGCACTTGGCGGTGAGCGCGTTC 1140
Qy      381 ArgArgGLnSerGLYValIIEGLYHisAspGLIuAspAsnGLYAsnValLeuArgAlaIIE 400
Db      1141 CCGCCGAGTCTGGGTGATCGGTCAAGCAAGCAACGCGCAACGTGTGCTGCGATC 1200
Qy      401 GIUPHPRGARGIIEIYAGIYLYSPROPHEAENIIEASPHRTPPHEANSER 420
Db      1201 GAGTTTCCCGCATCAAGGCGGCAACCGTTCAATGACACCGACTGGTTCAATGAC 1260
Qy      421 MetLeuSerGIuIleGIYnProLYSGLIYLYVAIGIuValSerHis 437
Db      1261 ATGTTGAGGAATCGGCCAGCTTAAGCGGTAAAGTGAAGTCAAGCCAC 1311

RESULT 7
US-10-321-210-15
; Sequence 15, Application US/10321210
; Publication No. US20040115657A1
; GENERAL INFORMATION:
; APPLICANT: Kofas, Matcheos
; APPLICANT: Odum, J. Martin
; APPLICANT: Norton, Kelley C.
; APPLICANT: Ye, Rick
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: C1619 US NA
; CURRENT APPLICATION NUMBER: US/10/321,210
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/934,901
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,906

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; PRIOR FILING DATE: September 1, 2000
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: METHYLOMONAS SP.
US-10-321-210-15

Alignment Scores:
Pred. No.: 4,086-253 Length: 1311
Score: 2284.00 Matches: 437
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-701-200-6 (1-437) x US-10-321-210-15 (1-1311)

QY 1 AspValValThrTrpProTyrHisLeuThrAlaAspIleAspPheCysHisTrpPhe 20
DB 1 GATGTGTCACATGGCCCTTATCACTTAACGGCTGATTCGATTTGTCATGGTTTTT 60
QY 21 LeuAspPheAspPheTyrThrLeuMetAspLysProLysValAlaIleLeuThrAla 40
DB 61 CTTAACCTTAACTTCTACACGCTCATACAACTTAAGTTGCAATACGACAGCA 120
QY 41 GlyGlyLeuAlaProCysLeuAsnSerAlaIleGlySerLeuIleGlyArgTyrThrGlu 60
DB 121 GGGCGCTTGGCGCTTGTGATTCGCAATCGGATGTTGATCGAAGCTTAACGGA 180
QY 61 IleAspProSerIleGlyIleIleCysTyrArgGlyGlyTyrLysGlyLeuLeuGly 80
DB 181 ATGATCTCTGACATAGAAATCATTTGCTATCGCGCGGTATTAAGCGCTGTGGGC 240
QY 81 AspSerTyrProValThrIleGluValArgLysValAlaGlyValLeuGluIleAspPheGly 100
DB 241 GATTTCTTATCATGACGCGCGGAGAGTCGTAAGAAAGCGGGGTGTCGCAACGTTTGGC 300
QY 101 GlySerValIleGlyAsnSerArgValLysLeuThrAsnValLysAspCysValLysArg 120
DB 301 GGTTCGTGATCGGCAACGCGCGGTCAATTAAGCAATGCAAAAGCTCGTGAAGAGC 360
QY 121 GlyLeuValLysGlyGlyGluAspProGluLysValAlaIleAspGluLeuValLysAsp 140
DB 361 GGTTTGGTCAAGGGGTGAAGATCCCAAAAGCTCCGCTGATCAATTGTTAAGAT 420
QY 141 GlyValAspIleLeuHisThrIleGlyGlyAspAspThrAsnThrAlaAlaIleAspLeu 160
DB 421 GGTGTCTATATTCGACACCATTCGGCGGAGATGATACCAATACGGCAGCGGGAATTG 480
QY 161 AlaAlaPheLeuAlaArgAsnAsnTyrGlyLeuThrValIleGlyLeuProLysThrVal 180
DB 481 GCAGCATTCCTGGCGCAAAATTAATTACGACTGACGCTCATTTGTTAACTTAACGCTC 540
QY 181 AspAsnAspValPheProIleLysGluSerLeuGlyAlaTrpThrAlaAlaGluGlnGly 200
DB 541 GATTAACGACGATTTTCGATCAAGCAATCACTAGCTCTTGACCTGCGCGGCAAGGC 600
QY 201 AlaArgTyrPheMetAsnValAlaIleGluAsnAsnAlaAsnProArgMetLeuIleVal 220
DB 601 GCGGTTATTTTCATGAACGTGGTGCCGAAACCAACCCCAACGACGATGATGTA 660
QY 221 HisGluValMetGlyArgAsnCysGlyTyrLysLeuThrAlaAlaThrAlaGlnGlyTyrArg 240
DB 661 CACGAAGTGAATGGCGCTGAACCTGGCTGACCGCTGCAACCGCGGAGGAATATCGC 720
QY 241 LysLeuLeuAspArgAlaGluTrpLeuProGluLeuGlyLeuThrArgGluSerTyrGlu 260
DB 721 AAATTACTGACCTGCGAGTGTTCGCGAATTTGGGTTGACTCTGTGATCTTAAGAA 780
QY 261 ValHisAlaValPheValProGluMetAlaIleAspLeuGluAlaGluAlaLysArgLeu 280
```

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DB 781 GTCGACGCGGTATTCCTCCGGAATGGCGATCGACCTGGAACCGGACGCGCTG 840
QY 281 ArgGluValMetAspLysValAlaAspCysValAlaIlePheValSerGluGlyAlaGlyVal 300
DB 841 CGCGAAGTGAATGACAAAGTCGATTCGTCACATCTCTGTTCCAAAGGTGCGCGCTC 900
QY 301 GluAlaIleValAlaGluMetGlnAlaLysGlyGlnGluValProArgAspAlaPheGly 320
DB 901 GAACTATCGTCCGGAATAGCAGGCGCAAGGCGCAGAGATGCGCGCATGCGTTCGCG 960
QY 321 HisIleLysLeuAspAlaValAlaAsnProGlyLysTrpPheGlyGluGlnPheAlaGlnMet 340
DB 961 CACATCAACTGATCGGTCGACACCTCGTAATGTGTGCGGACGCAATTCGCGAGATG 1020
QY 341 IleGlyValAlaLysThrLeuValGlnLysSerGlyTyrPheAlaArgAlaSerAlaSer 360
DB 1021 ATAGCGCGGGAATAAACCCGCTGTAACAAATCGGATTAATCCCGCTGCTTCGCTTCC 1080
QY 361 AsnValAspAspPheArgLeuIleLysSerCysAlaAspLeuAlaGluCysAlaPhe 380
DB 1081 AACGTTGACGACATGCGTTGATCAATCTGCGCGACTTGGCGGTGAGTCCGCTTC 1140
QY 381 ArgArgGluSerGlyValIleGlyHisAspGluAspAsnGlyAsnValLeuArgAlaIle 400
DB 1141 CGCCGCGAGTCTGGCGTGAATCGGTCAACGAGCAAGACGCGCAACGTTGGCGTGCATC 1200
QY 401 GluPheProArgIleLysGlyGlyLysProPheAsnIleAspThrAspTrpPheAsnSer 420
DB 1201 GAGTTCCGCGCATCAAGGCGGCAAAACGTTCAATATCGACACCACTGTTCAATAGC 1260
QY 421 MetLeuSerGluIleGlyGlnProLysGlyGlyValGluValSerHis 437
DB 1261 ATGTTAGCGAATCGCGCAGCTTAAGGCGTAAGTCAAGTCAAGCCAC 1311

RESULT 8
US-10-369-493-38035
; Sequence 38035. Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38035
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38035

Alignment Scores:
Pred. No.: 4,66-66 Length: 552
Score: 659.00 Matches: 125
Percent Similarity: 82.61% Conservative: 27
Best Local Similarity: 67.93% Mismatches: 32
Query Match: 28.85% Indels: 0
DB: 17 Gaps: 0

US-10-701-200-6 (1-437) x US-10-369-493-38035 (1-552)

QY 33 LysLeuValAlaIleLeuThrAlaGlyGlyLeuAlaProCysLeuAsnSerAlaIleGly 52
DB 1 CAGAAAGTCGACATGTCGACCGCGGTGCGCTCGCCCTGTCTCTTGGCGCGGTG 60
QY 53 SerLeuIleGluLysArgTyrThrGluIleAspProSerIleGluIleIleCysTyrArgGly 72
```









/ APPLICANT: SAKAKI, YOSHIYUKI  
 / APPLICANT: HATTORI, MASAHIRA  
 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 / FILE REFERENCE: 249-262  
 / CURRENT APPLICATION NUMBER: US/10/156,761  
 / PRIOR FILING DATE: 2002-05-29  
 / PRIOR APPLICATION NUMBER: JP 2001-204089  
 / PRIOR FILING DATE: 2001-05-30  
 / PRIOR APPLICATION NUMBER: JP 2001-272697  
 / NUMBER OF SEQ ID NOS: 15109  
 / SEQ ID NO 6060  
 / LENGTH: 1026  
 / TYPE: DNA  
 / ORGANISM: Streptomyces avermitilis  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (1)..(1026)  
 US-10-156-761-6060

## Alignment Scores:

Pred. No.:	1,576-23	Length:	1026
Score:	294.00	Matches:	101
Percent Similarity:	43.83%	Conservative:	66
Best Local Similarity:	26.51%	Mismatches:	140
Query Match:	15	Indels:	74
DB:		Gaps:	17

US-10-701-200-6 (1-437) x US-10-156-761-6060 (1-1026)

QY 34 LysValAlaIleLeuThrAlaGlyLeuAlaProCysLeuAsnSerAlaIleGlySer 53  
 DB 4 CGGGTGGAGTACTGACCGGAGGCGGAGCTGCCCGGGCTCAACCGCTCATCCGGGGC 63  
 QY 54 LeuIleGluArgTyrThrGluIleAspProSerIleGluIleCysTyrArgGly 73  
 DB 64 GTCTGCTCGTAAGCGCTGCAG--GAGTACGCTACGACTTCTCGGCTTCCGGGACGGC 120  
 QY 74 TyrLysGlyLeuLeuLeuGlyAspSerTyrProValThrAlaGluValArgLysValAla 93  
 DB 121 TGGGGGAGACCTCGAAGCGAGCC--GTCGGCTGCACATCCCGCGGTGGC 174  
 QY 94 GlyValLeuGlnArgPheGlyGlySerValIleGlyAsnSerArgValLysLeuThrAsn 113  
 DB 175 GGCATCTGCGCCCG--GGCGCAGATCTCGGCTCTCGCGGACCAACCCCTCAG 231  
 QY 114 ValLysAspCysValLysArgGlyLeuValLysGlyGluAspProGlnLysValAla 133  
 DB 232 CTCGACGAGCGCATCCGCGG--ATCCAGAG-- 261  
 QY 134 AlaAspGlnLeuValLysAspGlyValAspIleLeuHisThrIleGlyGlyAspAspThr 153  
 DB 262 ----AACTCCCAAGCAGAGGTGACGCGCTCATCGCGAGCGGCGGAGHACAG 315  
 QY 154 AsnThrAlaAlaIleAspLeuAlaAlaPheLeuAlaArgAsnAsnTyrGlyLeuThrVal 173  
 DB 316 CTCGGCGTGGCGGACGCGCTCAC--GACGAGTACGCGCGTGGCGGCTC 360  
 QY 174 IleGlyLeuProLysThrValAspAsnAspValPheProIleLysGlnSerIleGlyAla 193  
 DB 361 GTCGGGGTCCCGAAGCATCGACCAACGACTCTCGGCCACCGACTACGCTTCGCTTC 420  
 QY 194 TrpThrAlaAlaGluGlnGlyAlaArgTyrPhe-----MetAsnValValAlaGluAsn 211  
 DB 421 GACACGGCGGTGGCATTCGCGAGCGCATGACCGCTCCACACACCGCGCGAGTTC 480  
 QY 212 AsnAlaAsnProArgMetLeuIleValHisGluValMetGlyArgAsnCysGlyTyrPleu 231  
 DB 481 CACATCGCGC-----GTCTGCTGTGCGAGGTATGGCGCGGACCGGCGCTGATC 531  
 QY 232 ThrAlaAlaThrAlaGlnGlyTyrArgLysLeuLeuAspArgAlaGluTyrPleuProGlu 251  
 DB 532 GCCATCCACTCG----- 543

QY 252 LeuGlyLeuThrArgGlySerTyrGluValHisAlaValPheValProGluMetAlaIle 271  
 DB 544 ---GGCTTGGCGGGCGGCGC-----AACGTCATCTCTATCCCGAGCAGCGCTTC 591  
 QY 272 AspLeuGluAlaGluAlaLysArgLeuArgGluValMetAspLysValAspCysValAsn 291  
 DB 592 GACGTCAACAGGTGCGGCTATGTGACCTCGCGGTTCAAGCGCTCGTACCGCGGATC 651  
 QY 292 IlePheValSerGluGlyValArgLysValAlaIleValAlaGluMetGlnAlaLysGly 311  
 DB 652 GTGTGCTGCGCGAGGCGCG-----ATGCCAAGACCGC 687  
 QY 312 GlnGluValProArg-----AspAlaPheGlyHisIleLysLeuAspAlaVal 327  
 DB 688 CAGATGCTCTCAAGACGAGATCCCTCACTCTCTCGGACAGCTGCGCTTCGCGGGGTC 747  
 QY 328 AsnProGlyLysTyrPheGlyGluGlnPheAlaGlnMetIleGlyValAlaGlu--LysThr 346  
 DB 748 ----GGGAGTGGCTGGCGCAAGAGATCGAAGAGCGCACCGGCAAGAGGCGCGCAC 801  
 QY 347 LeuValGlnLysSerGlyTyrPheAlaArgAlaSerAlaSerAsnValAspAspMetArg 366  
 DB 802 ACGGTC-----CTCGGCGATGTGCAGCGCGGCGGACCGGACCGGCGCTTCGACCGCTGG 855  
 QY 367 LeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPheArgArgGlySerGlyVal 386  
 DB 856 CTCGCCACCCCGCTTGGCGCTGCACGCCCATCGAGCGGCTC----- 894  
 QY 387 IleGlyHisAspGluAspAsnGlyAsnVal-----LeuArgAlaIleGluPheProArg 404  
 DB 895 ----CGGACGCGGACCTTCGCAAGATGTGCGCTTCGCGGCGGACGAGCATCGTCCGT 948  
 QY 405 Ile 405  
 DB 949 GTC 951  
 RESULT 12  
 US-10-425-114-9204  
 / Sequence 9204, Application US/10425114  
 / Publication No. US20040034888A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Liu, Jindong  
 / APPLICANT: Zhou, Yihua  
 / APPLICANT: Kovalic, David K.  
 / APPLICANT: Screen, Steven E.  
 / APPLICANT: Tabaska, Jack B.  
 / APPLICANT: Cao, Yongwei  
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 / FILE REFERENCE: 38-21(5313)B  
 / CURRENT APPLICATION NUMBER: US/10/425,114  
 / NUMBER OF SEQ ID NOS: 73128  
 / SEQ ID NO 9204  
 / LENGTH: 1570  
 / TYPE: DNA  
 / ORGANISM: Glycine max  
 / FEATURE:  
 / OTHER INFORMATION: Clone ID: 700837684\_FLI  
 US-10-425-114-9204

Alignment Scores:  
 Pred. No.: 3,836-23  
 Score: 293.00  
 Percent Similarity: 41.23%  
 Best Local Similarity: 26.78%  
 Query Match: 17  
 DB: 15

US-10-701-200-6 (1-437) x US-10-425-114-9204 (1-1570)  
 QY 34 LysValAlaIleLeuThrAlaGlyLeuAlaProCysLeuAsnSerAlaIleGlySer 53

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Db 224 CAGGCTGCTATTGTTACTTGTGGGGGCTGTGTCCTGGCTCAACACTGTCATTAGGAA 283
Qy 54 LeuIIleGluArGyTrhGluIIleArpProSerIIleGluIIleCyStrArGlyGly 73
Db 284 TTAGTGTGGCTTACACCATATGTATGGGTGAGAGAGTTCTTGGAATCAATGGGGA 343
Qy 74 TyTrleGlyLeuLeuLeuGlyArpSerTrProValThrAlaGluValAlaGlyLysVala 93
Db 344 TATAGGGGTTTCTATGCTGGCAATACATCACTTAAACCCCT-----AAAAGTGTG 394
Qy 94 GlyValleuGlnArpRheGlyIySerValIIleGlyAsnSerArGyValIyLeuThrAsn 113
Db 395 AATGATATACATAAGCTGGGGGAACGTCTCGGAACATCAGA----- 439
Qy 114 ValIyArpCyValIyArGlyLeuValIyGluGlyGluArpProGlnIyValAla 133
Db 440 -----GTTGACATGACACCAAAAAGATV--- 463
Qy 134 AlaArpGlnLeuValIyArpGlyValAlaRplleuEnIleThrIIleGlyIyArpArpThr 153
Db 464 GTTGACAGTATTCAGATCGGGGATCATCAGTTTATTAATGGAGAGATGGAACT 523
Qy 154 AsnThrAlaAlaArpLeuAlaAlaRheLeuAlaArpAsnTrGlyLeuThrVal 173
Db 524 CAGAAGGTCATCTGCATTTTGGAGAGTCAGAAAGCTGTCTCAAGTTTCACT 583
Qy 174 IIleGlyLeuProIyThrValArpArpArpValRheProIIleIyGlnSerLeuGlyAla 193
Db 584 GTAGGTATCCCAAAACCATAGATTAATGATATTCAGATTGATTAAGCTTTTGGCTT 643
Qy 194 TrpThrAlaAlaGluGlnGlyAlaArGyTrPheMetAsnValAlaAlaGluAsnAla 213
Db 644 GACACTGCTTTGAGAGGCTCAACAGCTAATAAGTCACACATGTTGAAGTAAAGT 703
Qy 214 AsnProArpMetLeuIIleValIIleGluValIleMetGlyArpAsnCyStrIyLeuThrAla 233
Db 704 GTGAAATATGCATAGCTGTTCATCACTGATGGTGAAACAGCCGATTTATTCGA--- 760
Qy 234 AleThrAlaGlnIyTrArGlyLeuLeuArpArGlaGluTrIleuProGlnLeuGly 253
Db 761 -----ATGAT 766
Qy 254 LeuThrArpGluSerTrGlyValAlaAlaAlaRheValProGluMetAlaIIleArpLeu 273
Db 767 GCTACTCTTGCAGTGCAGAGCTGATGTGCTTAATTCAGAGTCACCCCTTTTACCTT 826
Qy 274 GluAlaGluAla-----LysArpLeuArpGluValIleMetArpLys 286
Db 827 GAAAGTCTGTGCTGATCTATGAATATATAGAGAAAGACTTAAAGAAATGGGCACATG 886
Qy 287 ValArpCyValAlaRplleRheValSerGlyValAlaGlyValAlaAlaIleValAlaGlu 306
Db 887 GTT-----ATTGTTATGTCTGAGAGCAGACAGACAGACTTGTTCGACAGT 934
Qy 307 MetGlnAlaIySerGlnIyValProArpArpAlaRheGlyAlaIleIyLysLeuArpAla 326
Db 935 GTGCAAGTCCATGCAAAACA-----GATGCTTCTGAAACAAGCTTTTTCAGAT 985
Qy 327 ValAsnProGlyIyTrPheGlyGlyGlnIleRheAlaGlnMetIIleGlyAlaGlyLysTrh 346
Db 986 GTT-----GGCTATGGATATCCCAAAAGATTAGGATCATTTTGTCTGCACAGAAACA 1039
Qy 347 Leu-----ValGlnLysSerGlyTrPheAlaArpAlaSerAlaSerAsp 361
Db 1040 CTGGCCATATCTCAATATCATATGATCCAACTATATGATCCGAGCTATTCACAGCAAT 1099
Qy 362 ValArpArpMetArpGluIleIySerCyAlaArpLeuAlaValGluCyAlaRheArp 381
Db 1100 GCCTGTGACAAAGCTGATGACACATTTCTGCTAAAGTCAAGTCTATGAGCAATG--- 1156
Qy 382 ArgGluSerGlyValIIleGlyLysArpGluArp-----AsnGluAsnValIleuArGla 399

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Db 1157 -----GCAAGTTACACTGGCTATACAAAGTGAAGCTTGATGAATGAAGA---CAAACTTAT 1207
Qy 400 IIleGluPheProArGlyIleIySerGlyLysProPheAsnIIleArpThrArp-----Trp 417
Db 1208 ATACCTCTTATATGATCACTGAGACAGAAACACAGTAGATATATGATGATGATG 1267
Qy 418 PheAsnSerMetLeuSerGluIIleGlyGlnPro-----LysGlyGlyLys 432
Db 1268 GCTAGG---CTTTATCTTCAACAATCAACCAAGCTTTTGGATGCCAAGGTTGACAT 1324
Qy 433 ValGlu 434
Db 1325 GAAAG 1330

RESULT 13
US-10-425-114-6293
; Sequence 6293, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6293
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700559917_FLI
US-10-425-114-6293

Alignment Scores:
Pred. No.: 4,55e-23 Length: 1765
Score: 293.00 Matches: 113
Percent Similarity: 41.23% Conservative: 61
Best Local Similarity: 26.78% Mismatches: 174
Query Match: 12.83% Indels: 74
DB: 17 Gaps: 15

US-10-701-200-6 (1-437) x US-10-425-114-6293 (1-1765)
Qy 34 LysValAlaIIleuThrAlaGlyIyLeuAlaRplleuProCyLeuAsnSerAlaIIleGlySer 53
Db 371 CAGGCTGCTATTGTTACTTGTGGGGGCTGTGTCCTGGCTCAACACTGTCATTAGGAA 430
Qy 54 LeuIIleGluArGyTrhGluIIleArpProSerIIleGluIIleCyStrArGlyGly 73
Db 431 TTAGTGTGGCTTACACCATATGTATGGGTGAGAGAGTTCTTGGAATCAATGGGGA 490
Qy 74 TyTrleGlyLeuLeuLeuGlyArpSerTrProValThrAlaGluValAlaGlyLysVala 93
Db 491 TATAGGGGTTTCTATGCTGGCAATACATCACTTAAACCCCT-----AAAAGTGTG 541
Qy 94 GlyValleuGlnArpRheGlyIySerValIIleGlyAsnSerArGyValIyLeuThrAsn 113
Db 542 AATGATATACATAAGCTGGGGGAACGTCTCGGAACATCAGA----- 586
Qy 114 ValIyArpCyValIyArGlyLeuValIyGluGlyGluArpProGlnIyValAla 133
Db 587 -----GTTGACATGACACCAAAAAGATV--- 610
Qy 134 AlaArpGlnLeuValIyArpGlyValAlaRplleuEnIleThrIIleGlyIyArpArpThr 153
Db 611 GTTGACAGTATTCAGATCGGGGATCATCAGTTTATTAATGATTAAGCTTTTGGACT 670

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QY 274 GluAlaGluAla-----LysArgLeuArgGluValMetAspLys 286  
DB 1166 GAAGGCTCTGGTGAAGCTTATATATAGAGAAAAGCTAAAGAAATGGGACATG 1225  
QY 287 ValAspCysValAsnIlePheValSerGluGluValAlaGluAlaIleValAlaGlu 306  
DB 1226 GTT-----ATTGTTATTTCTGGAAGGAGCAGAGACAGTCTTGTTCGAGACT 1273  
QY 307 MetGlnAlaLysGluGluGluValProArgAspAlaPheGluYhiIleLysLeuAspAla 326  
DB 1274 GTCCAGTCCATGAGCAAAACA-----GATGCTTCTGGAACAAGCTTTTCAAGAT 1324  
QY 327 ValAsnProGluYhiSerPheGluGluGlnPheAlaGlnMetIleGluValAlaGluYhiTrp 346  
DB 1325 GTT-----GGCTATGGATATATCCCAAAAGATTAGGAGATCTTTGCTGACGAAGACA 1378  
QY 347 Leu-----ValGlnLysSerGluYhiTrpPheAlaArgAlaSerAlaSerAsn 361  
DB 1379 CTGCCCATATCTCTCAAAATACATAGATCCAACTATATGATCCGAGCTATTCCAGCAAT 1438  
QY 362 ValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPheArg 381  
DB 1439 GCCTCTGACAAAGCTGTACTGACACACTTCTGCAAGTGCAGATTCTATGAGCAATG--- 1495  
QY 382 ArgGluSerGluValIleGluYhiLeuArgLysAsp-----AsnGluAsnValIleuArgAla 399  
DB 1496 -----GCAGGTATACACTGGCTATACAAAGTGAGCTTGTGAATGAGA---CAAACTTAT 1546  
QY 400 IleGluPheProArgIleLysGluYhiLysProPheAsnIleAspThrAsp-----Trp 417  
DB 1547 ATACCTCTTATATGAATCACTGAGAGACAGAACCAACAGCTAGTATGATGATGAATGTGG 1606  
QY 418 PheAsnSerMetLeuSerGluIleGluYhiPro-----LysGluYhiLys 432  
DB 1607 GCTAGG---CTTTATCTTCAACAAATCAACACCGCTTTTGGATGCCAAGGTGACAAAT 1663  
QY 433 ValGlu 434  
DB 1664 GAAGAG 1669

RESULT 15  
US-10-424-599-141147  
/ Sequence 141147, Application US/10424599  
/ Publication No. US20040031072A1  
/ GENERAL INFORMATION:  
/ APPLICANT: La Roga Thomas J  
/ APPLICANT: Kovalic David K  
/ APPLICANT: Zhou Yihua  
/ APPLICANT: Cao Yongwei  
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
/ FILE REFERENCE: 38-21(53223)B  
/ CURRENT APPLICATION NUMBER: US/10/424,599  
/ NUMBER OF SEQ. ID NOS: 285684  
/ SEQ. ID NO 141147  
/ LENGTH: 4413  
/ TYPE: DNA  
/ ORGANISM: Glycine max  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: PAT\_MRT3847\_98468C.1  
US-10-424-599-141147

Alignment Scores:  
Pred. No.: 1,74e-22 Length: 4413  
Score: 293.00 Matches: 113  
Percent Similarity: 41.23% Conservative: 61  
Beet Local Similarity: 26.78% Mismatches: 174  
Query Match: 12.83% Indels: 74  
DB: 17 Gaps: 15

US-10-701-200-6 (1-437) x US-10-424-599-141147 (1-4413)

QY 34 LysValAlaIleLeuThrAlaGluYhiLeuAlaProCysLeuAsnSerAlaIleGluSer 53  
DB 2954 CAGCTCTATATGTATCTTGTGAGGGCTGTGCTCGGGCTCAACCTGTCAATAGGCA 3013  
QY 54 LeuIleGluArgTrpThrGluIleAspProSerIleGluIleIleCysTrpArgGluYhi 73  
DB 3014 TTAGTGTGGCTTACACATATGATGTGGGGTGAAGAAAGTTCTTGGAATCAATGAGCA 3073  
QY 74 TyrLysGluLeuLeuLeuGluYhiAspSerTrpProValThrAlaGluValAlaGluYhiVala 93  
DB 3074 TATAGGGGTTTCTATCTGCAATACATCACTTAAACCCCT-----AAAAGTGTG 3124  
QY 94 GluValLeuGlnAlaArgPheGluYhiGluSerValIleGluYhiAsnSerArgValLysLeuThrAsn 113  
DB 3125 AATGATATACATTAAGGTGGGGAACCTGCTCGGAACATCAAGA----- 3169  
QY 114 ValLysAspCysValLysArgGluLeuValLysGluGluYhiLysAspProGlnLysValAla 133  
DB 3170 -----GGTGACATGACACCAAAAAGATA--- 3193  
QY 134 AlaAspGlnLeuValLysAspGluYhiLysIleLeuIleThrIleGluYhiAspAspThr 153  
DB 3194 GTTGACAGTATTCAGATGCGGGAATCAATCAAGTTATATATATGAGAGATGGAACAT 3253  
QY 154 AsnThrAlaAlaAlaAspLeuAlaAlaPheLeuAlaAlaArgAsnAsnTrpGluYhiLeuThrVal 173  
DB 3254 CAGAAAGGTGCACTTCATCTTCAATTTTGAAGAACTAGAAAGCTGTCTCAAAAGTTTACGTT 3313  
QY 174 IleGluPheProArgTrpValAspAsnAspValPheProIleLysGlnSerLeuGluYhiAla 193  
DB 3314 GTAGATATCCCAAAACCATATATATGATATTCAGATTATGATATTAAGCTTTGGCTTT 3373  
QY 194 TrpThrAlaAlaGluGlnGluYhiAlaArgTrpPheMetAsnValAlaAlaGluAsnAla 213  
DB 3374 GACACTGCTGTTGAGAGAGGCTCAACGAGCTATTAATGACAGACATGTGAAGCTGAAGT 3433  
QY 214 AsnProArgMetLeuIleValIleGluValMetGluYhiArgAsnCysGluYhiTrpLeuThrAla 233  
DB 3434 GTAGAAATATGCGATAGGTGTGTTCAGATTGATGTGTAAGAAACGGGATTTATATGCA--- 3490  
QY 234 AlaThrAlaGlnGluYhiArgLysLeuLeuAspArgAlaGluYhiTrpLeuProGluLeuGlu 253  
DB 3491 -----ATGTAT 3496  
QY 254 LeuThrArgGluSerTrpGluValIleValAlaPheValProGluMetAlaIleAspLeu 273  
DB 3497 GCTACTCTTGGCAGTGCAGACGATGTGCTTAAATTCAGAGTACACCTTTTACCTT 3556  
QY 274 GluAlaGluAla-----LysArgLeuArgGluValMetAspLys 286  
DB 3557 GAAGGCTCTGGTGAAGCTTATATATAGAGAAAAGCTAAAGAAATGGGACATG 3616  
QY 287 ValAspCysValAsnIlePheValSerGluGluValAlaGluAlaIleValAlaGlu 306  
DB 3617 GTT-----ATTGTTATTTCTGGAAGGAGCAGAGACAGTCTTGTTCGAGACT 3664  
QY 307 MetGlnAlaLysGluGluGluValProArgAspAlaPheGluYhiIleLysLeuAspAla 326  
DB 3665 GTCCAGTCCATGAGCAAAACA-----GATGCTTCTGGAACAAGCTTTTCAAGAT 3715  
QY 327 ValAsnProGluYhiSerPheGluGluGlnPheAlaGlnMetIleGluValAlaGluYhiTrp 346  
DB 3716 GTT-----GGCTATGGATATCCCAAAAGATTAGGAGATCTTTGCTGACGAAGACA 3769  
QY 347 Leu-----ValGlnLysSerGluYhiTrpPheAlaArgAlaSerAlaSerAsn 361  
DB 3770 CTGCCCATATCTCTCAAAATACATAGATCCAACTATATGATCCGAGCTATTCCAGCAAT 3829  
QY 362 ValAspAspMetArgLeuIleLysSerCysAlaAspLeuAlaValGluCysAlaPheArg 381  
DB 3830 GCCTCTGACAAAGCTGTACTGACACACTTCTGCTCAAGTGCAGATTCTATGAGCAATG--- 3886

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          ::|||      |||::|
Db      3887 -----GCAGGTTACACTGGCTATACAGTGCACCTTGATGAAAGAGA---CAAACCTTAT 3937
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Qy      400 IleGluPheProArgIleLysGlyLysProPheAsnIleAspThrAsp-----Tyr 417
          |||      |||      |||      |||
Db      3938 ATACCTTCTTATAGATCACTGAGAGACAGAACCACTAGTAGTATAGTAAATGTGG 3997
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Qy      418 PheAsnSerMetLeuSerGluIleGlyGlnPro-----LysGlyGlyLys 432
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Db      3998 GCTAGG--CTTTATCTTCACAAATCAACCCAGCTTTTGGATGCCAAGGGTGACAAAT 4054
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Qy      433 ValGlu 434
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Db      4055 GAAGAG 4060
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Search completed: March 31, 2005, 14:39:11  
Job time : 9183 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 09:56:53 ; Search time 1162 Seconds  
(without alignments)  
124.704 Million cell updates/sec

Title: US-10-701-200-6  
Perfect score: 2284  
Sequence: 1 DVTWPHYLTDIRFCHEMF.....FNSMSEIGOPKGVESH 437

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2284	100.0	437	9	US-09-934-901-16
2	2284	100.0	437	9	US-09-934-868-6
3	2284	100.0	437	10	US-09-941-947A-2*
4	2284	100.0	437	14	US-10-320-924-16
5	2284	100.0	437	14	US-10-320-874-16
6	2284	100.0	437	15	US-10-363-567-2
7	2284	100.0	437	16	US-10-321-210-16
8	659	28.9	184	15	US-10-369-493-14348
9	306.5	13.4	350	15	US-10-156-761-13510
10	294	12.9	342	14	US-10-425-114-44512
11	293	12.8	414	15	US-10-425-114-44512
12	293	12.8	525	15	US-10-425-114-44512
13	293	12.8	527	15	US-10-424-599-283989

14	293	12.8	527	15	US-10-425-114-49830	Sequence 49830, A
15	284.5	12.5	341	14	US-10-156-761-14652	Sequence 14652, A
16	279.5	12.2	603	16	US-10-437-963-204464	Sequence 204464, A
17	270	11.8	448	15	US-10-282-122A-47251	Sequence 47251, A
18	269.5	11.8	341	14	US-10-156-761-10359	Sequence 10359, A
19	269.5	11.8	530	16	US-10-767-701-46418	Sequence 46418, A
20	263.5	11.5	769	16	US-10-437-963-114757	Sequence 114757, A
21	261	11.4	345	15	US-10-369-493-19261	Sequence 19261, A
22	259	11.3	541	16	US-10-437-963-108835	Sequence 108835, A
23	255	11.2	434	15	US-10-425-114-43593	Sequence 43593, A
24	254	11.1	507	15	US-10-424-599-271108	Sequence 271108, A
25	253	11.1	319	15	US-10-369-493-2205	Sequence 2205, A
26	250.5	11.0	357	15	US-10-369-493-9669	Sequence 9669, A
27	248	10.9	447	15	US-10-424-599-211067	Sequence 211067, A
28	246.5	10.8	987	16	US-10-369-493-21998	Sequence 21998, A
29	246.5	10.8	987	16	US-10-477-369-41	Sequence 41, A
30	241.5	10.6	428	15	US-10-425-114-52834	Sequence 52834, A
31	241.5	10.6	481	15	US-10-424-599-258809	Sequence 258809, A
32	240.5	10.5	320	9	US-09-815-242-13785	Sequence 13785, A
33	240.5	10.5	320	15	US-10-282-122A-72968	Sequence 72968, A
34	240.5	10.5	320	15	US-10-282-122A-75033	Sequence 75033, A
35	240.5	10.5	320	15	US-10-282-122A-76025	Sequence 76025, A
36	239.5	10.5	318	15	US-10-369-493-9652	Sequence 9652, A
37	238.5	10.4	320	9	US-09-815-242-10422	Sequence 10422, A
38	238.5	10.4	320	15	US-10-369-493-23638	Sequence 23638, A
39	238.5	10.4	320	15	US-10-282-122A-56771	Sequence 56771, A
40	235	10.3	352	15	US-10-425-114-44609	Sequence 44609, A
41	234.5	10.3	327	15	US-10-282-122A-78090	Sequence 78090, A
42	232	10.2	461	15	US-10-282-122A-76398	Sequence 76398, A
43	229.5	10.0	295	15	US-10-369-493-8855	Sequence 8855, A
44	229.5	10.0	320	15	US-10-282-122A-56380	Sequence 56380, A
45	227.5	10.0	449	15	US-10-369-493-8876	Sequence 8876, A

ALIGNMENTS

RESULT 1  
US-09-934-901-16  
Sequence 16, Application US/09934901  
Patent No. US20020110885A1  
GENERAL INFORMATION:  
APPLICANT: Koffas, Matheos  
APPLICANT: Odum, J. Martin  
APPLICANT: NO. US20020110885A1ton, Kelley C.  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/09/934, 901  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229, 906  
PRIOR FILING DATE: September 1, 2000  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 16  
LENGTH: 437  
TYPE: PR  
ORGANISM: METHYLOMONAS SP.  
US-09-934-901-16

Query Match 100.0% ; Score 2284 ; DB 9 ; Length 437 ;  
Best Local Similarity 100.0% ; Pred. No. 4,9e+207 ;  
Matches 437 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;  
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DB 1 DVTWPHYLTDIRFCHEMFLLNFFYTLNKKPKVAIITAGIAPCLNSAIGSLIRYTE 60  
QY 1 IDPSIITICRGYKGLIGDSYPAFAVRKKAQVQRRGSGVIGSRVKTNTVKKCVRR 120  
DB 61 IDPSIITICRGYKGLIGDSYPAFAVRKKAQVQRRGSGVIGSRVKTNTVKKCVRR 120  
QY 121 GLVKEGEDPQKVAADLVKDGVDIILHTIGGDDTNTAAADLAFLARNNYGLTVIGLPKTV 180

DB 121 GLVKEEDPQKVAADLVKDGVDILHTIGDDTNTAAADLAFLARNNGTLVIGLPKTV 180  
QY 181 DNDVFPFKOSLGAMTAAGOGARYFNNVVAENNANPRLIVHEVMGNCMLTAATAOEYR 240  
DB 181 DNDVFPFKOSLGAMTAAGOGARYFNNVVAENNANPRLIVHEVMGNCMLTAATAOEYR 240  
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DB 241 KLIDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMKVDVCNIFVSEAGV 300  
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DB 301 EAIIVAEOMAKGOEVPBRDAFGHILKDAVNPCKMFGEOFAQMGIAEKTLYOKSGYFARASAS 360  
QY 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
QY 421 MLESIGOPKGGKVEVSH 437  
DB 421 MLESIGOPKGGKVEVSH 437

## RESULT 2

US-09-934-868-6  
Sequence 6, Application US/09934868  
Patent No. US20020137190A1  
GENERAL INFORMATION:  
APPLICANT: Koffas, Mattheos  
APPLICANT: Odum, James M  
APPLICANT: Schenzle, Andreas J  
TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1596 US NA  
CURRENT APPLICATION NUMBER: US/09/934,868  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,858  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 6  
LENGTH: 437  
TYPE: PRF  
ORGANISM: METHYLOMONAS SP.  
US-09-934-868-6

Query Match 100.0%; Score 2284; DB 9; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.9e-207;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 DNDVFPFKOSLGAMTAAGOGARYFNNVVAENNANPRLIVHEVMGNCMLTAATAOEYR 240  
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DB 301 EAIIVAEOMAKGOEVPBRDAFGHILKDAVNPCKMFGEOFAQMGIAEKTLYOKSGYFARASAS 360

QY 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
QY 421 MLESIGOPKGGKVEVSH 437  
DB 421 MLESIGOPKGGKVEVSH 437

## RESULT 3

US-09-941-947A-2  
Sequence 2, Application US/09941947A  
Publication No. US20030003528A1  
GENERAL INFORMATION:  
APPLICANT: Brzostowicz, Patricia C.  
APPLICANT: Cheng, Qiong  
APPLICANT: DiCosimo, Deana J.  
APPLICANT: Koffas, Mattheos  
APPLICANT: Miller, Edward S. Jr.  
APPLICANT: Odum, J. Martin  
APPLICANT: Picataggio, Steve  
APPLICANT: Rovierte, Pierre E.  
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE  
FILE REFERENCE: CL1903 US NA  
CURRENT APPLICATION NUMBER: US/09/941,947A  
CURRENT FILING DATE: 2001-09-01  
PRIOR APPLICATION NUMBER: 60/229,907  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,858  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 2  
LENGTH: 437  
TYPE: PRF  
ORGANISM: Methylomonas 16a  
US-09-941-947A-2

Query Match 100.0%; Score 2284; DB 10; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.9e-207;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DVTWTPYHLTADIRFCHEWFFLNFNFTYTLNKKPKVAIITAGGLAPCLNSAIGSLIERYTE 60  
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DB 121 GLVKEGEDPQKVAADLVKDGVDILHTIGDDTNTAAADLAFLARNNGTLVIGLPKTV 180  
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DB 181 DNDVFPFKOSLGAMTAAGOGARYFNNVVAENNANPRLIVHEVMGNCMLTAATAOEYR 240  
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DB 241 KLIDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMKVDVCNIFVSEAGV 300  
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DB 301 EAIIVAEOMAKGOEVPBRDAFGHILKDAVNPCKMFGEOFAQMGIAEKTLYOKSGYFARASAS 360  
QY 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
DB 361 NVDDMLIKSCADLAVECAFRRRESGVIGHDEBNGVLAIEFPRIKGRPFNIDTWFNS 420  
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DB 421 MLESIGOPKGGKVEVSH 437



Db 421 MLSEIQPKGKVEVSH 437

RESULT 4

US-10-320-924-16

Sequence 16, Application US/10320924

Publication No. US20030129721A1

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Odum, J. Martin

APPLICANT: No. US20030129721A1ton, Kelley C.

APPLICANT: Ye, Rick

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CL1619 US NA

CURRENT APPLICATION NUMBER: US/10/320,924

CURRENT FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US/09/934,901

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,906

PRIOR FILING DATE: September 1, 2000

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 16

LENGTH: 437

TYPE: PRT

ORGANISM: METHYLOMONAS SP.

US-10-320-924-16

Query Match 100.0%; Score 2284; DB 14; Length 437;

Best Local Similarity 100.0%; Pred. No. 4,9e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 IDPSIEIICYRGYKGLLDGSDYPVTAEVKKAQVLORFSGSVIGNSRVLTWVKDCVKR 120

Qy 121 GLYEGEDPQKVAADQVKGVDILHTIGGDDTNTAAADLAFLARNNGYGLTVIGLPKTV 180

Db 121 GLYEGEDPQKVAADQVKGVDILHTIGGDDTNTAAADLAFLARNNGYGLTVIGLPKTV 180

Qy 181 DNVPFPIKOSLGAMTAEOGARFPMNVVAENNANPRMLIVHEVMGRGCMLTAAAOEYR 240

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Db 241 KLDRAEWLPBELGLTRESYEVHAFVPEMAIDLEAEAKRLREVMKVDKVCNIFVSEAGV 300

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Db 301 EAIVAEQAKGQEVPRDAFGHIKLDVAVNPGKMFGEQFAQMI GAEKTLVQKSGYFARASAS 360

Qy 361 NVDDMLRIKSCADLAVECAFRRESGVIGHEDNGNVLRAIEFPRIKGGKPFNIDTWFNS 420

Db 361 NVDDMLRIKSCADLAVECAFRRESGVIGHEDNGNVLRAIEFPRIKGGKPFNIDTWFNS 420

Qy 421 MLSEIQPKGKVEVSH 437

Db 421 MLSEIQPKGKVEVSH 437

RESULT 5

US-10-320-874-16

Sequence 16, Application US/10320874

Publication No. US20030138909A1

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Odum, J. Martin

APPLICANT: No. US20030138909A1ton, Kelley C.

APPLICANT: Ye, Rick

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CL1619 US NA

CURRENT APPLICATION NUMBER: US/10/320,874

CURRENT FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US/09/934,901

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,906

PRIOR FILING DATE: September 1, 2000

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 16

LENGTH: 437

TYPE: PRT

ORGANISM: METHYLOMONAS SP.

US-10-320-874-16

Query Match 100.0%; Score 2284; DB 14; Length 437;

Best Local Similarity 100.0%; Pred. No. 4,9e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 IDPSIEIICYRGYKGLLDGSDYPVTAEVKKAQVLORFSGSVIGNSRVLTWVKDCVKR 120

Qy 121 GLYEGEDPQKVAADQVKGVDILHTIGGDDTNTAAADLAFLARNNGYGLTVIGLPKTV 180

Db 121 GLYEGEDPQKVAADQVKGVDILHTIGGDDTNTAAADLAFLARNNGYGLTVIGLPKTV 180

Qy 181 DNVPFPIKOSLGAMTAEOGARFPMNVVAENNANPRMLIVHEVMGRGCMLTAAAOEYR 240

Db 181 DNVPFPIKOSLGAMTAEOGARFPMNVVAENNANPRMLIVHEVMGRGCMLTAAAOEYR 240

Qy 241 KLDRAEWLPBELGLTRESYEVHAFVPEMAIDLEAEAKRLREVMKVDKVCNIFVSEAGV 300

Db 241 KLDRAEWLPBELGLTRESYEVHAFVPEMAIDLEAEAKRLREVMKVDKVCNIFVSEAGV 300

Qy 301 EAIVAEQAKGQEVPRDAFGHIKLDVAVNPGKMFGEQFAQMI GAEKTLVQKSGYFARASAS 360

Db 301 EAIVAEQAKGQEVPRDAFGHIKLDVAVNPGKMFGEQFAQMI GAEKTLVQKSGYFARASAS 360

Qy 361 NVDDMLRIKSCADLAVECAFRRESGVIGHEDNGNVLRAIEFPRIKGGKPFNIDTWFNS 420

Db 361 NVDDMLRIKSCADLAVECAFRRESGVIGHEDNGNVLRAIEFPRIKGGKPFNIDTWFNS 420

Qy 421 MLSEIQPKGKVEVSH 437

Db 421 MLSEIQPKGKVEVSH 437

RESULT 6

US-10-363-567-2

Sequence 2, Application US/10363567

Publication No. US20040077068A1

GENERAL INFORMATION:

APPLICANT: E.I. du Pont de Nemours & Company

TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

FILE REFERENCE: CL1903 PCT

CURRENT APPLICATION NUMBER: US/10/363,567

CURRENT FILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: US 60/229858

PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: US 60/229907

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 437

TYPE: PRT

ORGANISM: Methylobionas 16a  
US-10-363-567-2

Query Match 100.0%; Score 2284; DB 15; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.9e-207;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 DNDVFPFKOSLGAMTAAEGGARYFMNVVAENNANPMLIVHEVMGRNCMLTAATQOYR 240
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DB 241 KLLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVNI FVSGAGV 300
QY 301 EAIVAEMQAKGQVPRDAFGHILKDAVNPCKMFGQFQOMIGAETLVOKSGYFAPASAS 360
DB 301 EAIVAEMQAKGQVPRDAFGHILKDAVNPCKMFGQFQOMIGAETLVOKSGYFAPASAS 360
QY 361 NVDDMKLISKADLAVECAFRRESGVIGHDEDNGVLRALIEPRIKGKPFNIDTWFNS 420
DB 361 NVDDMKLISKADLAVECAFRRESGVIGHDEDNGVLRALIEPRIKGKPFNIDTWFNS 420
QY 421 MLSEIGQPKGKVEVSH 437
DB 421 MLSEIGQPKGKVEVSH 437
```

## RESULT 7

US-10-321-210-16  
Sequence 16, Application US/10321210  
Publication No. US20040115657A1  
GENERAL INFORMATION:  
APPLICANT: Koffaas, Mattheos  
APPLICANT: Odom, J. Martin  
APPLICANT: Norton, Kelley C.  
APPLICANT: Ye, Rick  
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN  
FILE REFERENCE: CL1619 US NA  
CURRENT APPLICATION NUMBER: US/10/321,210  
PRIOR FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US/09/934,901  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/229,906  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 16  
LENGTH: 437  
TYPE: PRT  
ORGANISM: METHYLOMONAS SP.  
US-10-321-210-16

Query Match 100.0%; Score 2284; DB 15; Length 437;  
Best Local Similarity 100.0%; Pred. No. 4.9e-207;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DVTWTFYHLTADIRFCWFFLNFFYTLNKKPKKVALITAGGLAPCLNSAIGSLIRYTE 60
DB 1 DVTWTFYHLTADIRFCWFFLNFFYTLNKKPKKVALITAGGLAPCLNSAIGSLIRYTE 60
```

```
QY 61 IDPSIEITICRGYKGLLDGSDYPVTAEVKKAQVLRFGSGVIGNSRVKLTNVKDCVR 120
DB 61 IDPSIEITICRGYKGLLDGSDYPVTAEVKKAQVLRFGSGVIGNSRVKLTNVKDCVR 120
QY 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTKV 180
DB 121 GLVKEGEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTKV 180
QY 181 DNDVFPFKOSLGAMTAAEGGARYFMNVVAENNANPMLIVHEVMGRNCMLTAATQOYR 240
DB 181 DNDVFPFKOSLGAMTAAEGGARYFMNVVAENNANPMLIVHEVMGRNCMLTAATQOYR 240
QY 241 KLLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVNI FVSGAGV 300
DB 241 KLLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVNI FVSGAGV 300
QY 301 EAIVAEMQAKGQVPRDAFGHILKDAVNPCKMFGQFQOMIGAETLVOKSGYFAPASAS 360
DB 301 EAIVAEMQAKGQVPRDAFGHILKDAVNPCKMFGQFQOMIGAETLVOKSGYFAPASAS 360
QY 361 NVDDMKLISKADLAVECAFRRESGVIGHDEDNGVLRALIEPRIKGKPFNIDTWFNS 420
DB 361 NVDDMKLISKADLAVECAFRRESGVIGHDEDNGVLRALIEPRIKGKPFNIDTWFNS 420
QY 421 MLSEIGQPKGKVEVSH 437
DB 421 MLSEIGQPKGKVEVSH 437
```

## RESULT 8

US-10-369-493-14348  
Sequence 14348, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 14348  
LENGTH: 184  
TYPE: PRT  
ORGANISM: Agrobacterium tumefaciens  
US-10-369-493-14348

Query Match 28.9%; Score 659; DB 15; Length 184;  
Best Local Similarity 67.9%; Pred. No. 7e-54; Indels 0; Gaps 0;  
Matches 125; Conservative 27; Mismatches 32;

```
QY 33 KKVAILITAGGLAPCLNSAIGSLIRYTEIDPSIEITICRGYKGLLDGSDYPVTAEVK 92
DB 1 QKVAILITAGGLAPCLNSAIGSLIRYTEIDPSIEITICRGYKGLLDGSDYPVTAEVK 92
QY 93 AGVLOPFGSGVIGNSRVKLTNVKDCVRKGLVKEGEDPQKVAADQVLDGVDILHTIGDD 152
DB 61 AHLHRYGSGPIGNSRVKLTNVKDCVRKGLVKEGEDPQKVAADQVLDGVDILHTIGDD 120
QY 153 TTTAAADLAFLANNYGLTVIGLPTVNDVFPFKOSLGAMTAAEGGARYFMNVVAENN 212
DB 121 TTTAAADLAFLANNYGLTVIGLPTVNDVFPFKOSLGAMTAAEGGARYFMNVVAENN 212
QY 213 ANPR 216
DB 181 ANPR 184
```





QY 327 VNEGKMFGEQFQMGAEKTL-----VQKSGYFARASASNVDMRLIKSCADLAVECAPR 381  
| : : : : :  
Db 377 V--GLWISQKIRHFAQAQKTLPTLKVDPTVMIRAIIPASASNVCTLLAQSAVHGAM- 433  
| : : : : :  
QY 382 RESGVIGHDED--NGNVLAIEPFRKKGKPFNIDTD--WFSNMLSEIGOP-----KGGK 432  
| : : : : :  
Db 434 --AGYGYTSGLVNCR-QTYIPFYRITERQNHVITDRMMAR--LLSTNQPSFLDAKGDN 489  
| : : : : :  
QY 433 VE 434  
| : : : : :  
Db 490 EE 491  
| : : : : :  
RESULT 14  
US-10-425-114-49830  
/ Sequence 49830, Application US/10425114  
/ Publication No. US20040034888A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Liu, Jinsong  
/ APPLICANT: Zhou, Yihua  
/ APPLICANT: Kovalic, David K.  
/ APPLICANT: Screen, Steven E.  
/ APPLICANT: Tabaska, Jack E.  
/ APPLICANT: Cao, Yongwei  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
/ FILE REFERENCE: 38-21(5313)B  
/ CURRENT APPLICATION NUMBER: US/10/425, 114  
/ CURRENT FILING DATE: 2003-04-28  
/ NUMBER OF SEQ ID NOS: 73128  
/ SEQ ID NO 49830  
/ LENGTH: 527  
/ TYPE: PRT  
/ ORGANISM: Glycine max  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: 700559917\_FLI.pcp  
US-10-425-114-49830  
Query Match 12.8%; Score 293; DB 15; Length 527;  
Best Local Similarity 26.8%; Pred. No. 1,3e-18;  
Matches 113; Conservative 61; Mismatches 174; Indels 74; Gaps 15;  
QY 34 KVAIITAGGLAPCLNSAIGSLIERYTEIDPSIEITICRGYKGLIGDSYPTVAEVRKA 93  
| : : : : :  
Db 124 QAAIVTCGGLCPBLNTVIRLVCGLHHMGVKVYLGINGSGRYARNTITLTP---KSV 180  
| : : : : :  
QY 94 GVLOFRGGSVIGNSRYKLTNVKDCVKRGLVKEGEDPQKVAADQLVKDGVDLHTIGDDT 153  
| : : : : :  
Db 181 NDHKKRGTVLGTSR-----GGHDTKKI--VDSIQBRGINQVYIIGDDT 223  
| : : : : :  
QY 154 NTAADLAFLAANNVGLTVIGLPTVNDVFPRIKQSLGAWTAEGCARFNNVVAENNA 213  
| : : : : :  
Db 224 QKASASIAFEEVRKGLKVSIVGIPKTIIDNDIPVIDSGFDPITVEEQRIINAAHVEAS 283  
| : : : : :  
QY 214 NPMMLIVHEVMGRNCGLTAATQAEYRKLLDRAEWLPELGLTRESYEVAHVPEMAIDL 273  
| : : : : :  
Db 284 VENGIGVVKLMGNSGIIA-----MYATLASRDVDCCLIPESFYI 324  
| : : : : :  
QY 274 EABA-----KRLREYMDKVDVNI FVSEGAVEAIVAEQAKGQEVPRDAFGH KIDA 326  
| : : : : :  
Db 325 EGGGGLYEYIEKRLKENGHNV-----IVIAEGAGDELVSBSVQMSKQ---DASGNKLFQD 377  
| : : : : :  
QY 327 VNEGKMFGEQFQMGAEKTL-----VQKSGYFARASASNVDMRLIKSCADLAVECAPR 381  
| : : : : :  
Db 378 V--GLWISQKIRHFAQAQKTLPTLKVDPTVMIRAIIPASASNVCTLLAQSAVHGAM- 434  
| : : : : :  
QY 382 RESGVIGHDED--NGNVLAIEPFRKKGKPFNIDTD--WFSNMLSEIGOP-----KGGK 432  
| : : : : :  
Db 435 --AGYGYTSGLVNCR-QTYIPFYRITERQNHVITDRMMAR--LLSTNQPSFLDAKGDN 490  
| : : : : :  
QY 433 VE 434  
| : : : : :  
433 VE 434

Db 491 EE 492  
RESULT 15  
US-10-156-761-14652  
/ Sequence 14652, Application US/10156761  
/ Publication No. US20030119018A1  
/ GENERAL INFORMATION:  
/ APPLICANT: OMURA, SATOSHI  
/ APPLICANT: IKEDA, HARUO  
/ APPLICANT: ISHIKAWA, JUN  
/ APPLICANT: HORIKAWA, HIROSHI  
/ APPLICANT: SHIBA, TADAYOSHI  
/ APPLICANT: SAKAKI, YOSHIYUKI  
/ APPLICANT: HATTORI, MASAHIRA  
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
/ FILE REFERENCE: 249-262  
/ CURRENT APPLICATION NUMBER: US/10/156, 761  
/ CURRENT FILING DATE: 2002-05-29  
/ PRIOR APPLICATION NUMBER: JP 2001-204089  
/ PRIOR FILING DATE: 2001-05-30  
/ PRIOR APPLICATION NUMBER: JP 2001-272697  
/ PRIOR FILING DATE: 2001-08-02  
/ NUMBER OF SEQ ID NOS: 15109  
/ SEQ ID NO 14652  
/ LENGTH: 341  
/ TYPE: PRT  
/ ORGANISM: Streptomyces avermitilis  
US-10-156-761-14652  
Query Match 12.5%; Score 284.5; DB 14; Length 341;  
Best Local Similarity 27.5%; Pred. No. 4.6e-18;  
Matches 97; Conservative 62; Mismatches 143; Indels 51; Gaps 11;  
QY 34 KVAIITAGGLAPCLNSAIGSLIERYTEIDPSIEITICRGYKGLIGDSYPTVAEVRKA 93  
| : : : : :  
Db 2 RIGVLTSGBDCCPLNATVIRSVVNR--AVVDHGDVIGFRDGMKGLLECDY--LKLDDVAVS 58  
| : : : : :  
QY 94 GVLOFRGGSVIGNSRYKLTNVKDCVKRGLVKEGEDPQKVAADQLVKDGVDLHTIGDDT 153  
| : : : : :  
Db 59 GILAR--GGTILSSRQVPHLRDGYER-----ARGHVAELGDAIIPIGSGT 105  
| : : : : :  
QY 154 NTAADLAFLAANNVGLTVIGLPTVNDVFPRIKQSLGAWTAEGCARFNNVVAENNA 213  
| : : : : :  
Db 106 LKAAARL-----SDAGLPIVGVPKTIIDNDIAVTDTFPGDPAVGVAATEALDRKTTAS 159  
| : : : : :  
QY 214 NPMMLIVHEVMGRNCGLTAATQAEYRKLLDRAEWLPELGLTRESYEVAHVPEMAIDL 273  
| : : : : :  
Db 160 HQRLIV--EVMGRHTGMIALHSGM-----AAGAHAIIVPERPFI 198  
| : : : : :  
QY 274 EBAKRLREYMDKVDVNI FV--SEGAVEAIVAEQAKGQEVPRDAFGH KIDAVNPKW 332  
| : : : : :  
Db 199 EELAAVGERFEFGKRFATVAAEGAKPRGSMDF---DEGKKDVGHERFAGI--ARK 252  
| : : : : :  
QY 333 FGEQFQMGAEKTLVQKSGYFARASASNVDMRLIKSCADLAVECAPRREG 385  
| : : : : :  
Db 253 LSLLEBERLKEKRPV--ILGHVQRGSTPTAAYRVLATRFGMAHVAEVNHGFE 304  
| : : : : :  
253 LSLLEBERLKEKRPV--ILGHVQRGSTPTAAYRVLATRFGMAHVAEVNHGFE 304

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Job time : 1164 secs

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